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AX01952 Homo sapi
BC033143 Homo sapi
AX535029 Sequence
AX535090 Sequence
CQ177675 Sequence
AL552304 Homo sapi
BC006890 Mus muscu
BC079148 Rattus no
AL627228 Mouse DNA
AC05579 Rattus no
AC118963 Rattus no
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AC126312 Rattus no
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AC18569 Sequence
AX535028 Sequence
                                                                  March 11, 2006, 19:43:27 ; Search time 8477 Seconds (without alignments) 11486.709 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                            OM nucleic - nucleic search, using sw model
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Direct Submission
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
Kernalisgenomics@hri.co.jp, Tel:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Bconomy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5- & 3-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
RAB; annotation: HRI and RAB.
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LLQVYC"
                                                                                                                                                                Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Fukuzumi, Y., Sato, H., Wakamatu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagateuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., NBOD human cDNA sequencing project
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Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satch, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21, 243 full-length
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Best Local Similarity 99.9%;
Matches 1694; Conservative (
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                                                                                             human cDNAs
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/trānslation="WGSSFGYPDVKLKGIPVYPYPRATSPADDADSCCKEPLADPPPM
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TSEGRSTRAAAPTAAADSGHETWVGSGLSQDELTVQISGETTADAIARKLRPYGAPG
YPASHDSSFQGTDTDSSGAPLLQVYC"
                                                                                                                                                                                                                                                                                                   Anticoboggac.bc.ca
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
Wong, Corey Matsuc, Jaclyn Baland, Susan Gibson, Luis delatho, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
Santos, Duane Smallus, Jeff Stott, Miranda Tsai, George Yang,
Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 43 Row: c Column: 17.
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   Submitted (25-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help death. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAGCAGCCGCCGCACCCGTAGACCAG
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cDNA Library Arrayed by: The I.MA.G.B. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/db_xrefe="GeneID:126695"
387. :1121
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99.8%; Pred. No. 0;
ive 0; Mismatches
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/protein_id="AAH33143.1"
/db_xref="G1:21619959"
/db_xref="GeneID:126695"
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                                  GGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCC 1409
                                                                                                                                                                                                                                                                                                                                                                           TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 1589
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                 TGCCTTGGCTGACTGCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC
                                                                                              TGCCTTGGCTGACTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC
                                                                                                                                                                                                                TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG
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1634 GGATCTACATCTCCTTGCATCCTGATCCTGATCCCTGGGGCCCCTTCCTT		AUTHORS MACINIA, N.A., Recipon, H., Chen, S.I., Sun, I. and Liu, C.  TITLE Compositions and methods relating to lung specific genes and JOURNAL Patent: WO 20068633.A 117 06-SEP-2002;  Bidexus, Inc. (US)  Location/Qualifiers  1. 1977  Rource  1. 1977  Corganism="Homo sapiens"  Anol_type="unassigned DNA"  Ab_xref="taxon:9606"  ORIGIN  Query Match  Query Match  93.5%; Score 1602.4; DB 6; Length 1977;  Best Local Similarity 99.0%; Pred. No. 0;  Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;	ATGCCCGGCCTGGACACCCCGGCCAGCATCAGGCCTCCAGGCTTGGGACCGTGGGAG 60
		ACCITATCAGGGATCACGGAGGATTAGGAGGATGAGGATGAGGAGTAGGAGGGCGCC IS ACCITATCAGGAGCTCACGAGGACCGCC IS TGGTACGGGGCATCATCAGGACTAGGAGAGGAGGAGTGCTGGGGGCGCC IS TGGTACGGGGGCATCATTAGGAACCGGAAAGAGCGGTGCTCGCCCACAGACCTCGG 949 TGGTACGCGGGCATCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGG 121 AGGGTCGTTCAACTCGGCTGCTGCCCCACACCGCTGCTGCCCCTGACAGGCCATGAGA 100 AGGGTCGTTCAACTCGGCCCCAACCGCTGCTGCCCCTGACAGGGCCATGAGA 127 CCATGGTGGGCTCAGGCGTGCCCAGGAGACGAGAGAGAGA	1070 CTGCAGATCCATGGCCGGAAGCTTATGGAGCTCCAGGCAAGCC 1129  1134 CTGCAGATCCCATGGCCGGAAGCTGAGGCTTATGGAGCTCCAGGGAAGCC 1129  1130 ATGACTCATCCTCCAGGGCACCGACACACACTCGTCGGGGGCACCCTTGCTCCAGGTGT 1189  1130 ATGACTCATCCTTCCAGGGCACCGACACACACTCGTCGGGGGCACCCTTGCTCCAGGTGT 1189  1190 ACGCTAACCCTGCCAGGCCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAG 1249  1110 ACGCTAACCCCTGCCAGGCCCAGCTGCCACCCCTTTCTGGGAGAAGCATGGCCTACAG 1249  1111

1634   GGATCTACATCTCCTTGCATCCCAGCTGATCCCTGCCAGGGCCCCTTCCTT	2 5	Hominidae; Homo.  Hominidae; Homo.  HORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  LE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof  RNAL patent: WO 02068579-A 3609 06-SEP-2002;  PE Corporation (NY) (US)  RES Location/Qualifiers  Forgonism="Homo sapiens"  Amol Type="Lunassigned DNA"  And Type="Lunassigned DNA"	Match Local Similari es 1197; Cons 1 ATGCCCC 1 ATGCCCA 61 CGGCCAA 61 CGGCCAA 121 CGCACCA 121 CGCACCA 181 ATCTCTG
8 6 8 6 8 6 8 6 8	RESULT 7 CO11675 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL FEATURES	ORIGIN Ouery Best; Best; Oy Db Oy Db Oy Db
	651 TTCTTTCCATGACTGGACCTGCGAGATGGCCAGTGCCTCCATGTCCAGCGG 710		1010   CCATGGTGGGCTCAGGTCTCAGCABATGAGCTGACAGTTCTCCCAGGAGACGA   1059
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
Clon Jun 17, 2002 this sequence version replaced gi:20218554.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Dem:, EMB.; Sw., SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group, Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group. Further information. Constructed by the group http://www.sanger.ac.uk/HGP/Chri
RP11-344Hil is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see of Pieter de Jong. For further details see of Pieter de Jong. For further details see of Pieter group. VECTOR: pBACe3.6
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least once subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo. [ Dases 1 to 140207)
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//note="Sequence from overlapping clone RP4-633N17
(AL137860). Assembly confirmed by restriction digest."
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Homo sapiens (human)
Homo sapiens
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Contact: vega@sanger.ac.uk
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KEYWORDS
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AL356390.24 GI:21436506
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                                                        CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG 360
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DEFINITION
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LLQVYC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82299 recercioses de destraces de contractor de contractor
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                                                                                                                 /gene="RFD1-344H11.3"
/locus tag="RP11-344H11.3-001"
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terminator reads only." R1757,84288. .84370)
      /note="match: cDNAs: Em:AK007551.1 Em:AK091952.1
Em:AX747274.1 Em:BC006890.1 Em:BC033143.1"
79656. .79827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ġ
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                                                                                                                                                                                                                                                          |oin(82059. .83097,83683. .83757,84288. .84370)
|gene="RP11-344H11.3"
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/product="nuclear distribution gene C homolog
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Pred. No. 1.9e-243;
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100.0%; Pred. No.....
0; Mismatches
   protein"
   product="novel
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Best Local Simil
Matches 1039; C
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/gene="RP11-44H11.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AARRYACLVTLHRVVNESTVCLMNHERRQTLDLIAALALQALAEQGPAATAALAWRPP
GTDGVVPATVNYYYTPVQPLLAHAYPTWLPCN"
29398. . 29408. . 24411.8"
/gene="RP11-344H11.8"
                                                                                                                                                                                                                                                                                                                        / translation="MPSESGAERDRAAQVGTAAATAVATAAPAGGGPDPEALSAFP
GRHLSGLSWPQVKRLDALLSEPIPIHGRGNFPTLSVQPRQIVQVVRSTLEEQGLHVHS
VRLHGSBASHTHPESGLGYKDLDLVFRVDLRSEBASFQLTKAVVLACLLDFLPAGVSR
AKITPLTLEKAYVQKTKAAVYQKTSISISNKSGRAVELKFVDSVRRQFEFSIDSF
QIILDSLLLFQQCSSTUPKTSFAHPTVTGESISLSGKTGAFFLEHLHHRYIATRSPEBIRGG
GLLKYCHLLVRGFRPRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLBRHFGGAD
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Sw:P38061 Tr:AAH46339 Tr:AAP80706 Tr:BAC21646 Tr:BAC25812
Tr:C0509375 Tr:C060373 Tr:C229280 Tr:CBC177 Tr:C986C50
Tr:C0817D3 Tr:C96UVG1 Tr:C90VTG Tr:C9TTX8"
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/locus tag="RP11-344H11.4-001"
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Tr:AAM68299 Tr:CAAL156 Tr:RAA13967 Tr:O60886 Tr:O7ZUG1
Tr:Q862X1 Tr:Q8AVW0 Tr:Q8C2K0 Tr:Q90VV6 Tr:Q9NQ02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: ESTs: Em:A1435085.1 Em:BG752663.1
Em:BM021923.1 Em:BM682682.1 Em:BQ646324.1 Em:BQ892187.1
/gene="RP11-344H1.8"
/locus tag="RP11-344H1.8-001"
/standard name="OTHUMP0000004474"
/note="maEch: proteins: Tr:Q8C152 Tr:Q8C110 Tr:Q96A09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48099. .48542
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Tr:BAAL561 Tr:Q7ZWJ3 Tr:Q8TBU1 Tr:Q9CPZ2 Tr:Q9NRP0
Tr:Q9P075 Tr:Q9P1R4"
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/product="rithosomal protein L32 (RPL32) pseudogene"
complement(join(53464, .53610,53925, .54274))
/locus_tag="RP11-344H11.4-001"
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/product="ribosomal protein L12 (RPL12) pseudogene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tags"RPI1-344H11.8-001"
complement(join(33541. .34592,39827. .40731))
/locus tags"RPI1-344H11.7-001"
complement(join(33541. .34592,39827. .40731))
/locus tags"RPI1-344H11.7-001"
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                                                                                                                                                                                                                                                                                                -xref="UniProt/TrEMBL:Q96A09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (50415. .50811)
/locus_tag="RP11-344H11.5-001"
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/locus_tag="RP11-344H11.6-001"
/pseudo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .duct="novel pseudogene"
.xref="PSEUDO:CAI13556.1"
                                                                                                                                                                                            protein_id="CA113555.1"
|db_xref="G1:55959148"
|db_xref="Genew:28273"
                                                                                                                                                                    'product="novel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="RP11-344H11.8"
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                                                                                                                                  /codon start=1
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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q20
Insert size: 111138; sum-of-contigs
Insert size: 119403; 8.4% error; agarose-fp
Quality, coverage: 11.23x in Q20 bases; sum-of-contigs Quality
coverage: 10.67x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 1.2e-242;
0; Mismatches 2; Indels 0; Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18058: contig of 18058 bp in length
18059 18158: gap of 100 bp
18159 35144: contig of 16986 bp in length
1815 35244: gap of 100 bp
18245 54710: contig of 19466 bp in length
1811 72936: contig of 18126 bp in length
1813 73036: gap of 100 bp
1837 92888: contig of 1852 bp in length
1889 92888: gap of 100 bp
1889 108739: contig of 1855 bp in length
1840 111738: contig of 15751 bp in length
1840 111738: contig of 2899 bp in length.
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18159. 35144
fragment:02454
fragment chain:I"
35245. 54710
fragment chain:I"
400es assembly fragment:02786
fragment chain:I"
54811. 72936
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fragment chain:2"
73037. 22808
/note="assembly fragment:01820
fragment_chain:2"
92989. 108739
/note="assembly_fragment:01122
fragment_chain:2"
108840. 111738
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/note="assembly_fragment:02048
fragment_chain:1
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fragment_chain:2
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="1"
       Center project name: dJ426N7
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/clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_end:SP6
vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 60.5%;
Best Local Similarity 99.8%;
Matches 1037; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_end:T7
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Homo sapiens chromosome 1 clone RP3-426N7, 7 unordered pieces.
AL592304
GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 420
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92719 GAGTCGGACCTGGACCTGCCGGAGATGGCCAGTGGCCCCATGTCGAGCCGAGAATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
Center: Sanger Centre
Center: Sanger Centre
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                          82419 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCAGCCCTGATCGT
                                                                                                                 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
HOmo gapiens (human)
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/db_xref="taxon:10090"
/clone="MGC:11921 INAGE:3599314"
/clone="MGC:11921 INAGE:3599314"
/closue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
                 BC006890 1680 bp mRNA linear ROD 29-JUN-2004
Mus musculus RIKEN cDNA 1810019J16 gene, mRNA (cDNA clone MGC:11921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: p Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19526881. Location/Qualifiers
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Submitted (27-APR-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Prcurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                  IMAGE:3599314), complete cds.
                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
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/strain="FVB/N"
                                                                                                                BC006890.1 GI:13905189
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                                                                                                                                                                                          95846 CGCACCCGTAGACCCCAAGGACCCCTGGCCACCATGGGCCAGAGAGATACCTTC 95905
                                                                                                                                                                                                                                                                                       95966 TGGGTGTGGGAGTGGTGCCGGCCTTCTGCTTCCGCCGCCGCTGCCGGGATTGCCTCCAG 96025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96086 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 96145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96326 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 96385
  95726 AIGCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG 95785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96026 cGCTGTGGAGCCTGTGTGTGTGGGGATGCAGCCCTGCCTGTCTACTGAGGATTCCACTGAG 96085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACTGGCCCAGCAGTCACGGCCTCTCCTGGAAGAAGCATAGCCAGC----GGAGGAGAG 1303
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buerow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Gunarathe, P.H., Richards, S.,
Wockernan, K.J., Malek, J.A., Gunarathe, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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                           GTGCTTATTTTCAAGAAGCTGACAGAGCTGTTCAGCGTGCACCAGATTGACGAGCTGGCC
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VCPPARTVHPPAAGMKGSRPAMAAASATLMLSSKASLSTPTAMPPPGSLTWPPAARS
PWPSLLPHGTACLAPSPTAPAALRSTTPSMNRTWTCLRWAVAPCRAGRSTCLFSRS"
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llarity 82.3%; Pred. No. 9.5e-225;
Conservative 0; Mismatches 232;
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/product="RIKEN cDNA 1810019J16"
                        'note="Vector: pCMV-SPORT6'
                                                                                                                                                                                                                                                                                      /protein_id="AAH06890.1"
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/db_xref="MGI:1916323"
                                                                                /gene="1810019J16Rik"
/db_xref="GeneID:69073"
/db_xref="MGI:1916323"
                                                                                                                                                                      142. .792
/gene="1810019J16Rik"
host="DH10B"
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FHESDLDLPEMGSGSMSSREI DVLI FKKLTELFSVHQI DELAKCTSDTVFLEKTSKI S
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ETWYGSGLSQDELIVQISQETTADAIARKLRPYGAPGYPASQDSSPQGTDTDSSGAPL
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nford, CA 94305
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pdprdpghHGpesItFISGSAEPANEPPTCCLLwrpwGwDwCraaFCFRRCRDCLQRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACVRSCSPCLSAGDPIEGSSEAAWAKEHNGVPPSPDRAPPSRRDGQKLKTSMGSSFS
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                       WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: (Dickot, Mark) mcd@paxil.stanford.edu
Contact: (Dickot, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-MGG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: d Column: 16 This Clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /produci="similar to hypothetical protein FLJ34633"
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                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
//organism="Rattus norvegicus"
//db type="MRC:94165 IMAGE:7128510"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 935.8; DB 9;
Pred. No. 3.9e-218;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pExpressl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MGC94165"
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                                                                                                                                                                                                                                        Director MGC Project.
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ilarity 80.4%;
Conservative
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                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                   PUBMED
REFERENCE
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COMMENT
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Indels

Best Local Similarity Matches 1148; Conser

ATGCCCCGCCCTGGACACCCCCGCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG

1020 1080 1209 1032 1089 1140 096 540 900 780 840 912 900 972 180 252 240 312 300 372 CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG 360 432 420 492 480 552 612 672 099 732 720 792 852 313 TGGGGTTGGGACTGGTGTAGGGCTGCCTTCTGCTTCCGACGCTGCAGGGATTGCCTCCAG GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCCAGCCCTGATCGT TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA GAGTCGGACCTGGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT 733 GAATCGGACCTGGACCTGCCCGAAATGGGCAGTGGCTCCATGTCGAGCCGTGAGATCGAC 781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGC 901 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 973 ATCATCCGCATCAGTACCCGCAAAAGCCGCTCGCGGCCACAGACCTCTGAGGGGCGCTCA 961 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGC 1021 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCC 1090 rcredectreadecadeareaacreacadrecadarereceaagadacaaceeeagareee ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGTACCCAGCAAGCCATGACTCATCC CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCGC GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC GTGCTTATTTTCAAGAAGCTGACAGAGCTGTTCAGTGTACATCAGATTTGACGAGCTGGCC 133 AGGCCCACAGAGTIATGCCTGGAAACGAATGATGAGCGCTCCCAGCCCCCACCAGGCCGT GCACCCCCAGCCGGCGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC GCACCCCCCAGCCGCCGGGATGGCCAAAAGCTCAAGACCAGCATGGGCAGCTTCAGC AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 1081 원 Š

Mon Mar 13 12:24:33 2006

from the whole genome sh a phred quality of at le FEATURES Location/Qualif Source (1193813 Amol_type="geno"/Amol_type="	Query Match Best Local Similarity 85.8%; Pr Matches 891; Conservative 0;	103889	Db 103949 AGGCCATCAGAGTATATGCCTGG	Oy 121 CGCACCGTAGACCAGACCCA 	Oy 181 ATCTCTGGCTGAGCCGG	Oy 241 TGGGTGTGGGAGTGGTGCCGGG	Oy 301 CGCTGTGGAGCCTGTGCGGG	Oy 361 GGGACTGCTGAAGCCAACTGGG 	Oy 421 GCACCCCCAGCCGGGGGGGTG 	104369	bb 104429 GTCCTGAGGGAGTCTGGT	Oy 601 AGCCTGCCCAGCACCTTTGCCA 	Oy 661 GAGTCGGACTGGACTGCGGG 	Qy 721 GIGGICAICITCAAGAAGGIGA	Oy 781 AAGTGCACATCAGACACTGTGT	
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1141 1210 1201 1201 1261	Db 1328 AGGACCTCTGTGTGCAGGCCAGATTCTGAGCCCCAGAAGCAGTGACCTCTGTGGCTTGTGC 1387  Qy 1321 TGCCTTGGCTGACTGCGTTCCTGGACCATGTGCATTCACTGGGCCATGGGATCTACATC 1380  Db 1328 TTTTCTTCTTGCTGACTACTGTGTTCTTCACTGGGCCATGGGATCTACACTT 1380	1381 TCTTGCATCCCCAGCTGCATCCTGCCAGGGCCCCTTCCTT	RESULT 12 A.16.272.8	_	ACLESSION ALG27228.31 GI:28208155 KEYMORDS HTG. SOURCE Musculus (house mouse)		opkins, B. irect Submi ubmitted (C	Cambringsenite, Call 1554, OK. Befail and states: humquerydgenite, cac.uk Clone requests: clonerequestosac.uk COMMENT On Feb 4, 2003 this sequence version replaced gi:22474404.	Center: Metacode: SC Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk	During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission annotation the may not be found in the sequence submission.	corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:	Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.aanger.ac.uk/Projects/C elegans/wormpep This sequence	was integer as londows unless conservate notes: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as attempt and proper and problems, such as a sequence of the problems.	compressions and repeats; and regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.	<pre>RP23-13/122 IS Irom the RPC1-23 Mouse BAC Library constructed by the group of Pieter de Jong. FOr further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6</pre>	Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data

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SACCTTGAGTCCCCACCTGCTGCTCTCTGGCGACCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                336ATGCAGCCCTGCCTGTCTACTGAGGACTCCACTGAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33CCAAGGAGACAATGGAGTGCCCCCAGCCCTGATGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCTCGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 840
                                                                                                                                                                                                                         ACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC 780
shotgun alone has only been used where it has least 30.
ifiers
                                                                                                                                                                                                                                                             GAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC 120
                                                                                                                                                                                                                                                                                                             AAGGACCCTGGCCACCATGGGCCAGAGGCATTACCTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCAGCGCTCAAGTCAACCATGGCCAGCAGCTTCAGC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TECAAGGAGCCACTGGCCGATCCCCCACCCATGCGACAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720
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                                                                                                                                                                                                          CGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG 60
                                                                                                                                                                                  3; Gaps
                                                                                                                                                        Score 791; DB 9; Length 193813;
Pred. No. 1.1e-182;
Mismatches 145; Indels 3;
                                                     is musculus"
nomic DNA"
con:10090"
                                                                                                      137L22"
PCI-23"
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Submitted (199-NOV-2002) Human Gencem Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON Nov 9, 2002 this sequence version replaced gi:22772470.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.tuc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                          Worley.K.C.
Direct Submission

Burdet Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(Bases I to 235419)

Rat Genome Sequencing Consortium.

Direct Submission
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wo, T., Yakub, S., Yen, J., Yoon, U., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, X., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clohe name: CR230-11020
Assembly program: Phrap, version 0.990329
Consensus quality: 22536 bases at least Q40
Consensus quality: 227458 bases at least Q30
Consensus quality: 227458 bases at least Q30
Consensus quality: 228649 bases at least Q20
Estimated insert size: 2285433; aum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 221492: contig of 221492 bp in length 3 221592: gap of unknown length 3 22851: contig of 7059 bp in length 32 228751: gap of unknown length 52 235419: contig of 6668 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine Center code: BCM
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/mol_type="genomic DNA"
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/note="clone_boundary
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228752
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
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Rattub morregicus (Norway rat)

Rattub morregicus (Metazoa) (Chordata; Carniata; Vertebrata; Euteleostomi; Metazoa) (Chordata; Chires; Rodentia;

Sulvaryota; Metazoa; Chordata; Muridae; Murinae; Rattus

1 (Daesa 1 to 235419)

Salvaryota; Burdaria; Marchonteglires; Glitces; Rodentia;

1 (Daesa 1 to 235419)

Salvaria; Metazer, M. Lee, Abramaton; Adaden, Berahmed; F. Bladvin, D. Bandaranie, Metazer, M. Lee, Abramaton; Adaden, Berahmed; F. Bladvin, D. Bandaranie, D. Barber, M. Barnstead, M., Berahmed; F. Bladvin, D. Bandaranie, D. Barber, M. Barnstead, M., Eenahmed; F. Bladvin, D. Bandaranie, D. Barber, M. Barnstead, M., Eenahmed; F. Bladvin, D. Bandaranie, D. Barber, M. Barnstead, M., Eenahmed; F. Bladvin, D. Bandaranie, C., Cox, C., Coyle, M., Cree, A., D'Souza, L. Clavelond, C., Cockerl, R., Cox, C., Coyle, M., Cree, A., D'Souza, D. Dayland, C., Davy-Carroll, L., Davdar, M., Cree, M., Davis, C. Dedarich, D. Dalgado, O. Denson, S., Deramo, C., Dingy Y., Duhn, H., Divya, K., Davila, M., Bugene, C., Evans, C.A., Falls, T. Fan, G. Fernandaz, S., Filley, M., Eday, M., Gorbes, L., Foster, M., Gebregoorgis, B., Geer, K. Gall, R., Gardy, M., Guerra, W., Gebregoorgis, B., Geer, K., Gall, R., Gardy, M., Guerra, W., Gebregoorgis, B., Geer, K., Hade, S., Hadun, S. L., Hodgen, M., Harnin, C., Hamilton, C., Hamilton, K., Hannes, S., Hadun, S., Hune, J., Inday, M., Galler, D., Jacken, L., Ludou, M., Mallor, S., Kelly, S., McLeod, M., Mallor, M., Mallor, M., Martine, M., Martin
                                                                                                                                                                                                                                                                                                    104849 GCCGCTCTACTGCCC----CTGCTGCTGCCCCCGACAGTGGCCATGAGACCATGCTGGGC 104905
       104789 ATCATCCGTATTAGTACCCGCAAAAGCCGCTCCCGCCCACAGACCTCCGAGGGGCGCTCA 104848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACU95979 235419 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
                                                                                                                                                                                                                                                               961 ACTCGGGCTGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCATGAGAGCCATGGTGGGC 1020
                                                                                                                        901 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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	4; Length 235419; ; Indels 3; Gaps	:TCCACGCTTGGGACCGTGGGAG 	ACCTCAGCCCCCAAGCCGC                CTCCCAGCCCCACCAGGCCGT	TGGGCCAGAGAGCATTACCTTC	CTGCTGCCTGCTCTGGCGACCCCCCCCCCCCCCCCCCCC	CCGCTGCCGGGATTGCCTCCAG 	GTCTACTGAGGACTCCACTGAG                     ATCTGCTGGAGACCCCATTGAA	AGTGCCCCCCAGCCTGATCGT	DAACCATGGGCAGCAGCTTCAGC                     CAGCATGGGCAGCTTCAGC	CTACCCGAGGCCACCTCCCCA	CGATCCCCACCCATGCGACAC	CGAGGAGTACTATTCTTTCCAT	CATGTGAGCCGAGAAATTGAT 	ACACCAGATCGATGAGCTGGCC 	TPAGATCTCGGACCTTATCAGC 
end sequence:BH344795" 219911. 220573 7note="clone boundary clone end:Sp6 site:EcoRI end:sequence:BH344813" 221493221592 /estimated_length=unknown 228652228651	45.1%; Score 773.4; DB 14 ilarity 84.7%; Pred. No. 2.2e-178; Conservative 0; Mismatches 156;	1 ATGCCCGCCTGGACACCCCGCCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG	CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACGAAGCGC 	CGCACCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC	ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGCTTGGCGACCC	rgggrgrggaagrggrgggggggggggggggggggggg	CGCTGTGGAGCCTGTGTGGGGGAATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG 	GGBACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 	GCACCCCCAGCGGGGGGAIGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCAGCTTCAGC 	TACCCCGATGTTAAGGTCAAGGCATCCCTGTGTATCCCTACCGGAGGGCCACCTCCCCA	GCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCCACCCA	AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT	GAGTCGGACCTGGACGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAATTGAT 	GTGCTCATCTTCAAGAAGCTGACAGTTCAGCGTACACCGGATCGATGAGCTGGCC 	aagtecacatcagacactgtgttcctggagaagacagtaagatctcggaccttatcagc 
feature 215	h Sim 80;	1 ATGCCCCGCC	61 CGGCCAACAC 	121 CGCACCCGTR            83206 CGCACCCGG	181 ATCTCTGGCT              83266 ATTTCAGGCT	241 TGGGTGTGGG           83326 TGGGGTTGGC	301 CGCTGTGGAC           83386 CGCTGTGGAG		421 GCACCCCCC 	- 9	541 GCCCCTGATG                   3626 GTCCCTGACG	601 AGCCTGCCC           3686 AGCTTGCCT	661 GAGTCGGACC           3746 GAATCGGACC	721 GTGCTCATC7             806 GTGCTTATT7	781 AAGTGCACAT           3866 AAGTGCACAT
misc_f gap gap ORIGIN	Query Match Best Local Matches 88	93C	Oy Db 831	Oy 1	Oy 1	Oy 2 Db 833	Oy 33	Oy 361 Db 83446	Oy 4 Db 835	Cy 48 Db 8356	Oy 5	Qy 6 Db 836	Oy 6 0b 837	Oy 7	Oy 7

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Raktus norvegicus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mamalia, Butheria, Buarchonteglises, Gilres; Rodentia;
Sciurognathi; Murcides; Muridae; Murinae; Rattus.

Sciurognathi; Murcides; Murchae; Marchae; Rattus.

1 (Bases 1 to 249406)

Allen, A. Allen, H., Alabrooks, S., Amin, A., Angalano, D.,
Angalabechi, V., Aoyagi, A., Aydeli, W., Barnstead, M., Benammed, F.,
Blawalo, K., Blair, J., Blantenburg, E., Blyth, P., Brown, M.,
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Rotherbwart, M., Malu, Y., London, P., Longon, P., Lorensuba, W., Lut, M., Liu, W., Liu, Y., London, P., Loges, M., Mallos, S., Riggs, F.,
Mangum, B., Mapun P., Martin, K., Martin, R., Martine, S., Riggs, F.,
Rother, S., Paul, H., Perez, S., Socielle, R., Rose, M., Rose, S., Reville, M., Sodergren, S., Paul, H., Perez, S., Socielle, M.
249406 bp DNA linear HTG 15-NOV-2002 norvegicus clone CH230-180E4, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                        961 ACTCGGGCTGCTGCCCCAACCGCTGCTGCTGACAGTGGCCATGAGACCATGGTGGGCC 1020
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                                                                                                         AC118963
Rattus norvegicus clone CH230-180E4, WORKIN AC118963
AC118963.4 GI:25009106
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP. Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                GCACCCCCCAGCCGCCGGGATGGCAAAAGCTCAAGACCAGCATGGGCAGCAGCTTCAGC 14277
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                                                                                                                                  61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCCACCAAGCCGC
                                                                                                                                                                                                                                                                                                                                                              14576 ATTTCAGGCTCTGCAGAACCAGCCAACGAGCCCCCAACCTGCTGCCTCCTCTTGGCGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACCCCGATGTTAAGCTCAAAGGCATCCCTGTATCCCTACCCGAGGGCCACCTCCCCA
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                                              1 ATGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Daylor Plaza, Houston, TX 27030, USA Daylor Plaza, Daylor Plaza, Marian Sequence on this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* CONSIS: This is a "working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (122-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, D., Way, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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Pred. No. 2.2e-178;
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-180E4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 249406)
Rat Genome Sequencing Consortium
Direct Submission
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/note="wgs_contig"
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84.7%;
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                                                                                                                                     Direct Submission
Unpublished
                                                                                                                                                                                                         Worley, K.C.
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Best Local Similarity
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13740

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(http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 256017;
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22 83821: gap of unknown length
22 253567: contig of 169746 bp in length
25367: gap of unknown length
8 256017: contig of 2350 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bon.tmc.edu
Center project Information
Center project name: TUNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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6668. .7475
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clone_end:T7
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38358. .39527
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19978. .221353
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83722. .83821
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1 (Dasea 1 to 25601)

Saluzognachi, Murcidea, Muridea, Murinae, Rattus.

1 (Dasea 1 to 25601)

Mazury, D. M., Adams, C., Adio-Oduola, B., Ail-Osman, F. R., Allan, C., Anastunge, H.C., Arej. T., Ayele, M., Banks T., Barder, J., Burkel, C., Burch, E., Burch, P., Burkel, C., Burch, E., Burch, P., Burkel, C., Burch, E., Burch, F., Burkel, C., Burch, E., Burch, M., Bryatt, N. P., Buhay, C., Burch, P., Burkel, C., Burch, E., Burch, E., David, R., Datorae, S. R., Chacko, J., Chavez, D., Chen, Z., Chen, Z., Chodhyy I., Christopulos, C., Clen, G., Chen, Z., Chodhyy I., Christopulos, C., Chen, Z., Chen, Z., Chodhyy I., Christopulos, C., Chen, Z., Chen, Z., Chodhyy I., Christopulos, C., Davila, M., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Dutbhi, M., David, R., Davida, M., Carrer, M., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Dutbhi, K.J., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Dutbhi, K.J., Bollins, E., Garcia, A., Garcia, A., Garca, R., Garca, M., Garca, M., Garcia, A., Garca, M., Marca, G., Harris, K., Marca, G., Harris, K., Marca, G., Man, M., Marca, G., Man, M., Marca, G., Man, M., Marca, G., Mitchell, T., Marca, M., Marca, M.
                                                                                                                        AC126312 256017 bp DNA linear HTG 13-NOV-2002
Rattus norvegicus clone CH230-1B9, *** SEQUENCING IN PROGRESS ***,
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Search completed: March 11, 2006, 22:21:20

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 atgccccgccctggacaccc.....tacctcggccgcgaccacgc 1713 US-09-989-890-105 Perfect score: Sequence: Title:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4996997 segs, 3332346308 residues Searched:

9993994 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

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geneseqn2002as:\* geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs: geneseqn2003as:\* geneseqn2003bs:\* geneseqn2005s:\* geneseqn1980s:\* geneseqn1990s:\* N\_Geneseq\_21:\* 1: geneseqn198 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	•	Description	Abt13390 Breast sp	Add01260 Human nuc	Adb62645 Human cDN	Abx92075 Lung spec	Abx92014 Lung spec	Aea19545 Novel hum	Abt07645 Human bre	Aaz17414 Human gen	Abx92013 Lung spec	Abt07644 Human bre	Abt13389 Breast sp	Aaf64421 Novel hum	Aaf66376 Novel hum	Aaz13392 Human gen	Aax98308 Human can	Abx92074 Lung spec	Ada71938 Rice gene	Ada71938 Rice gene	Ada53405 Human cod
		ΩI	ABT13390	ADD01260	ADB62645	ABX92075	ABX92014	AEA19545	ABT07645	AAZ17414	ABX92013	ABT07644	ABT13389	AAF64421	AAF66376	AAZ13392	AAX98308	ABX92074	ADA71938	ADA71938	ADA53405
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		atch Length DB	1713	2392	1785	1977	1977	791	654	728	385	386	386	393	427	300	300	120	2000	2000	2761
de	Query	Match	100.0	98.9	98.8	93.5	93.5	44.5	35.5	27.0	22.5	22.2	22.2	20.6	20.3	17.5	17.4	7.0	3.4	2.8	2.7
		Score	1713	1694.6	1692.8	1602.4	1602.4	763	607.6	463.2	385	380.2	380.2	352.6	347	300	298.4	120	57.8	48.8	46.4
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Continuation (40 o Ach7772 Human gen Adg85607 Human tum Aa842190 Genomic a Aax54724 Human GM-Aa29293 Human GM-Ab295987 Human GM-Ab29638 Human low Abz96538 Human nuc Aax55274 Human fac Aax53491 Human fac Aax53491 Human eac Aaf21437 Human fac Aax63491 Human eac Aaf21437 Human fac Aax63491 Human eac Aaf21437 Human eac Aax63491 Human eac Aaf21437 Human eac Aaf21437 Human eac Aaf21437 Human eac Aaf46880 Human cys Adm85942 Human cys Adm85942 Human cys Adm85942 Human cys Adm85949 Human REM Aa82879 B Human REM Adm86840 Human REM ABB879 Polynucle	Adb31523 Human cDN Aba06478 Human cDN Abv83815 Human pol Adx33683 Piant ful Aca56890 Human sig Ad156686 Human pol
AA199683 39 ACH77772 ACH77772 ADQ85607 AAX542190 AAX54724 AAAX50293 AAAA34722 AAAA34722 AAAA34722 AAAA3437 AAX53491	ADB31523 ABA06478 ABV83815 ADX33683 ACA56890 ADI56686
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## ALIGNMENTS

Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer; metastatic; breast cancer; breast specific; human; ds. Breast specific related polynucleotide SEQ ID No 105. ABT13390 standard; DNA; 1713 BP. 21-NOV-2001; 2001WO-US043815. 22-NOV-2000; 2000US-0252509P. (first entry) (DIAD-) DIADEXUS INC WO200277232-A2 Homo sapiens. 30-JAN-2003 03-OCT-2002. ABT13390; 

Sun X, Macina RA, Recipon H, Pluta J, WPI; 2003-018927/01. Salceda S,

ΰ rin New isolated nucleic acid molecule, useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient.

Claim 1; Page 250-251; 377pp; English.

comprising: a sequence encoding a sequence comprising 11-1518 amino acids ; a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptic and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides The invention relates to a novel isolated nucleic acid molecule

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of the invention can be used to treat disorders by gene therapy. This polynucleotide represents a breast specific related sequence of the invention
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human; nucleic acid-associated protein; NAAP; cytostatic; antiarteriosclerotic; anti-HIV; antiallargic; cerebroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; antiparkinsonian; ophthalmological; thyromimetic; antiarthritic; hepatotropic; antibacterial; virucide; protozoacide; antiparasitic; fungicide; gene therapy; cell proliferative disease; cancer; atherosclerosis; hepatitis; neurological disorder; Parkinson's disease; Alzheimer's disease; stroke; epilepsy; developmental disorder; renal tubular acidosis; anaemia; glaucoma; hypothyroidism; Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes human nucleic acid-associated proteins designated NAAP-1 to NAAP-57. The human NAAPs have cytostatic, antiatreriosclerotic, antiathly, antiallergic, cerebroprotective, antiparkinsonian, anticonvulsant, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, thyromimetic, antiarthritic, antiparketrial, virucide, protocoacide, antiparsatitic and tengicide activities and can be used in diagnosing, treating and polymucleotide sequences can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative diseases (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. cancer, atherosclerosis, hepatitis), autoimmunef,inflammatory disorders (ADS, allergies, hypothyroidism), autoimmunef,inflammatory disorders (ADS, allergies, atopic dermatitis, arthritis) and infections (e.g. bacterial, viral, viral, atterior, and processed of the process
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human nucleic acid-associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
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Bmerling BM, Forsythe IJ, Gorvad AB, Griffin JA,
hare R, Lal PG, Lee RA, Lee SY, Li JX, Marquis JP;
Richardson TW, Sprague WW, Swarnakar A, Tang YT;
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autoimmune disorder; inflammatory disorder; AIDS; allergy; atopic dermatitis; arthritis; infection; gene; ss.
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98.9%; Score 1694.6;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1697; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; SEQ ID NO 98; 405pp; English
                                                                                                                                                                                                                                                                                                                                                             Azimzai Y, Baus.
Biliott VS, Emerling ...
"...hle AE, Khare R, Lal PG,
T. Richardson TW, Sprac
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                                                                                                                                                                                                                                     19-DEC-2001; 2001US-0343004P.
11-JAN-2002; 2002US-0347633P.
25-JAN-2002; 2002US-0351749P.
22-FEB-2002; 2002US-035949BP.
                                                                                                                                                                                               18-DEC-2002; 2002WO-US041115
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P-PSDB; ADD01203.
                                                                                                            WO2003054219-A2
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25-JAN-2002;
22-FEB-2002;
                                                                   Homo sapiens
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                                                                                                                                                                           TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1634
                                                1695 TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R, Tamechika I;
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                                                                TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG
                                                                                                                                           TCAACAGTTAAAAAGAAGCTTATTCTTAAATGTATTGTATTGGGGGGGTGGGCAGGCCCACT
                                                                                                                                                                                                                                                                                                                             Human; 88; gene; pharmaceutical; diagnostic; gene therapy;
tissue regeneration; cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
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Jai K, Irie F
Masuho Y;
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90. .1286
/*tsg= a /product= "Clone KIDNE20157100 protein"
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, M
                                                                                                                                                                                                                                                                                                             Human cDNA encoding clone KIDNE20157100
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Otsuka M,
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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2002US-00350978
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Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-450961/43.
P-PSDB; ADB64615.
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide or its partial peptide, immunologically assaying the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contexting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polypucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesishing the polynucleotide, or as a probe or proteins are useful as pharmaceutical agents and manocaded concept of proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related concept encoded proteins. The polynucleotide and encoded concept encoding them can be used as indicators for diseases (e.g. osteoporosis, transcription-related proteins, disease-related proteins and genes are involved in tissue and/or cell concoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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Claim 1; Page; 222pp; English
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Best Local Similarity 99.9%;
Matches 1694; Conservative
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The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosting, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists so of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, gene therapy, vaccine, lung specific antigen, cancer diagnosis, cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal; gene; ss.
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1249 1189 1369 1069 1129 1453 1513 1309 1633 1429 1693 1489 1549 1609 1669 1393 1753 1813 1873 1933 vulnerary; CNS-gen.; gene therapy; diagnostic; forensic; mapping; bNA purification; protein purification; osteoarthritis; antiarthritic; osteopathic; musculoskeletal disease; osteopathics; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy; Alzheimers disease; neuroprotective; nootropic; degeneration; parkinsons disease; antiparkinsonian; neurological disease; cerebrovascular ischemia; cerebroprotective; vasotropic; cardiovascular disease; autoimmune disease; immunosuppressive; immune diseace; viral infection; virucide; infection; cancer; 1454 ACTGCTAACCCCTGCCAGGCCCAGCTGCCATTCTGGGAAAGCATGGCCTACAG CTGGGTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATG 1574 CTGGTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGGATTCACTGGGCCATG 1694 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG 1754 AGTGAACCCTGATCCCCTATTGCCACCCTAACCAATGATGAAGTTCTCCCTC 1214 AGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCATGAGA 1274 CCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGA CTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCC CTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCCAGGTACCCAGGCAAGCC 1130 ATGACTCATCCTTCCAGGGCACCGACACAGACTCGTCGGGGGCACCCTTGCTCCAGGTGT 1190 ACTGCTAACCCCTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAAGCATGGCCTACAG 1250 AATGAAGAGGGGACCAGGAACCCCTGTGGGAGAGACTTAGACCTGAAGCAGTGCCCACT 1514 AATGAAGAGGGGACCAGGAACCCCTGTGGGAGAGCCTTAGACCTGAAGCAGTGCCACT GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG 1490 AGTGAACCCTGACTCCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTC CCTGGGGTAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATTGGGGGTGGG 1814 CCTGGGGTAATTCAACAGTTAAAAGAGCTTATCTTAAATGTATTGTATTGGGGGGGTGGG CAGGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT 1874 CAGGCCCACTCTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT CCATGGTGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGA 1670 CTTAACATGACCACAGTTTGTAAGTACCTCGGCGGCGACCACGC 1713 CTTAACATGACCACAGTTTGTAAGTACCTCGCTCGCGCGCCACGC 1977 Novel human polynucleotide SEQ ID NO 239

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Zhou P, Ma Y; Goodrich R, Chen R;

Ren F, Wang D,

Zhang J, Zhao Q, 1

Wang ZW, Asundi V,

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New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral
                                                                                          Wehrman T, Weng G, Boyle B;
                                             11-MAR-2004; 2004WO-US007412
                                                         14-MAR-2003; 2003US-00389559
cytostatic; neoplasm; gene;
                                                                                                     WPI; 2005-417730/42
                                                                              Wang J,
Xue A, A
                                                                    (NUVE-) NUVELO INC
                                                                                                           P-PSDB; AEA20112
                      WO2005049806-A2
           Homo sapiens.
                                  02-JUN-2005
                                                                               Tang TY,
Ghosh M,
                                                                                                                                                                                                                                                                                                                                       novel
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8 ద 8 셤 à 셤 ò 셤 ò 셤 ठे The invention describes a new isolated polymucleotide (I) encoding a polypeptide with biological activity comprising: a nucleotide sequence of SEQ INUIY defined); a nucleotide sequence that hybridizes to the sequence of (i) under stringent hybridization conditions; or a nucleotide sequence of (i). Also described are: a(n) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polymucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide of sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide of (3) and a sequence of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3) and a carrier; an antibody directed against the polypeptide of (3); a method of carrier; an antibody directed against the polypeptide of (3); and a carrier; an antibody directed against the polypeptide of (3); and a collypeptide of (3); and a collypeptide of (3); a method for identifying a compound that binds to the polypeptide of (3); and a collypeptide of (3); an exthod of producing the polypeptide of (3); and a collypeptide of SEQ ID NOS: 1-567 encoding a polypeptide of (3); and a collypeptide of (3); and a collypeptide of (3); and a collypeptide of of polymucleotides, where the collection of sequences and methods are useful in diagnostics, forensic, and gene mapping, in identifying of mutations responsible for genetic disorders or cher traits, in assessing biodiversity, and for producing many other types of data and products dependent on DNA and anino acid sequences. The composition and method are useful for treating a disease, burns, CNA and porture and products dependent on DNA and anino acid sequence. This sequence of caucoimmune disease, Alzheimer's disease, Parkinson's disease, parkingon's caucoimmune diseas 60 1 ATGCCCCGCCCTGGACACCCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG Gaps 5 Length 791; Sequence 791 BP; 149 A; 278 C; 222 G; 142 T; 0 U; 0 Other; Indels Score 763; DB 14; Pred. No. 7.1e-196; 0; Mismatches 0; Claim 1; SEQ ID NO 239; 500pp; English. polypeptide of the invention. Query Match
Best Local Similarity 99.7%;
Matches 785; Conservative infection, or cancer.

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180
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CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC
              120 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGATTACCTTC
                                                                                                                            240 TGGGTGTGGGGGGGGGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG
                                                                                                                                                                  CGCTGTGGAGCCTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG
                                                                                                                                                                                                                                                                                                                                                  480 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                         <u> AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT</u>
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                                                                                                                                                                                                                                                   360 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT
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                                                                                                                                                                                                                                                                              GCACCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC
                                                                                                                                                                                                                                                                                                                                   TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast cancer associated coding sequence SEQ ID NO: 124.
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(first entry)

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Human, gene, gene expression product, diagnosis, therapy, probe, detection, mapping, tissue typing, profiling, forensic, cancer, genetic analysis, colorectal cancer, breast cancer, lung cancer, 88.
                                                    Human gene expression product cDNA sequence SEQ ID NO:4887
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human genes and their expressed in different cell
                                                                                                                                                                                                                                                                                                                                                                                                                 Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-494092/41.
                          12-OCT-1999
                                                                                                                             Homo sapiens
                                                                                                                                                     WO9938972-A2
                                                                                                                                                                                                                                                                    03-APR-1998;
03-APR-1998;
21-OCT-1998;
28-OCT-1998;
                                                                                                                                                                                                       28-JAN-1999;
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31-MAR-1998
                                                                                                                                                                               05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                      Lamson G,
 AAZ17414;
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                                                                                                                                                                                                                                                                                                                                                                                      Reinhard
                                                                                                                                                                                                                                                                                                                                    (CHIR )
                                                                                                                                                                                                                                                                                                                                                  (HXSE-)
 The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                                            89 ATGATAAACCACCTCAGCCCCCACCAAGCCGCCGCACCGTAGACCAGGACCCCAAGGACC 148
                                                                                                                                                                                                                                                                                                                                                              CTGGCCACCATGGGCCAGGGCATTACCTTCATCTCTGGCTGCTGAGCCGGCCCTTG 208
                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCACAATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGGATGGCCA-- 446
                                                                                    New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                             CTGGCCACCATGGGGCCAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTG
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                         Cafferkey
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                          Karra K,
                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                       35.5%; Score 607.6; DB 6; 96.6%; Pred. No. 7.8e-154; tive 0; Mismatches 19;
                          Recipon H,
                                                                                                                                                                                                                                Sequence 654 BP; 118 A; 232 C; 186 G; 118
                                                                                                                                                                                                        sequence of the invention
                                                                                                                                        Claim 1; Page 248; 367pp; English.
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Matches 632; Conservative
                        S, Macina RA,
Liu C;
DIADEXUS INC
                                                              WPI; 2002-657582/70.
                                                                                                                                                                                                         coding
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expression products which are differentially types.

Labat I;

J, Innis MA, Garcia PD, Sudduth-Klinger Randazzo F, Kennedy GC, Pot D, Kaseam A, Crkvenjakov R, Dickson M, Drmanac S, Lab Garcia V, Jones WL, Stache-Crain B,

LT, Escobedo I C, Giese K, 3, Drmanac R, Escobedo

CHIRON CORP. HYSEQ INC.

98US-0072910P. 98US-0075954P. 98US-0080114P. 98US-008066EP. 98US-0105234P. 98US-0105234P.

99WO-US001619

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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell. comprising detecting at least one differentially expressed gene product in a test sample from a cell consecred of being cancerous, where the gene product is encoded by one of the polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensice, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two calls (e.g. to identify abnormal) or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnostis, prognosis and management of colorects, present cancer, and management of colorects cancer, and management of colorects cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 728 BP; 145 A; 190 C; 178 G; 150 T; 0 U; 65 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.0%; Score 463.2; DB 2; Length ilarity 88.4%; Pred. No. 1e-114; Conservative 0; Mismatches 66; Indels
Claim 1; Page 2323-2324; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide analogues and antagonists
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Best Local Similarity
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AAZ17414 standard; cDNA; 728

AAZ17414 ID AAZ1 XX RESULT

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cancer and non-cancerous diseases of the lung.
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                                                                                                                                                                                                                                                                                                                                AGTGCCCACTCTGGCTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCA 1359
                                                                                                                                                                                                                                                                                                                                                                             CTGGGCCATGGGATCTACATCTCCTTGCATCCCCAGGTCTGATCCCTGCCAGGGCCC 1419
                                                                                                                                        GGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCC 1121
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                                                                                                                                                     GGAGACGACTGCAGGTGCCATCGCCCGNAAGCTGAGGCCTTATGGAGCTCCAGGGTACCC 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
            151 GGGCCGGCTGGTACGCTGGATCATTCCCATAGINCCCGAAAGAGCCGTGCTTGGCNACA
                                                               CTCCAGGTGTACTGCTAACCCCTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAAAGCA
                                                                                                                                                                                                                                                                                                                                                      AGTGCCCACTCTGGNTCCTCNTGNCTTGGCTGGNTT-CTGGACCATGTGCATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                   CTGGNCCATGGGATCTACATCT-CTTGCATNCCCANCTGG--CTGATCCTGCCANGGNCC
                                              GACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGG
                                                                                          CCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer monitoring; cancer staging; cancer imaging; lung cancer, non-cancerous diseases of the lung; transgenic animal; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCTTCCTGCTCATGGTCTTCAGGTGGCCTGATCATGGAAAG 1463
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTNCNTCCTGCTCATGGNCTTNAGGNNGNCTGATCATNGAAAG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ວັ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung specific nucleic acid (LSNA) #55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX92013 standard; cDNA; 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-2001; 2001WO-US043612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIAD-) DIADEXUS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AGreAACCCreACCCATCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCTC 360
                                   The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-1421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, invention are useful for identifying uniq cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CTGGCTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1430 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG
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0
                                                                                                                                                                                                                                                                                                                                                                                                               Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                              Sequence 385 BP; 80 A; 122 C; 93 G; 90 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast cancer associated coding sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.5%; Score 385; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.2e-93;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1550 CCTGGGGTAATTCAACAGTTAAAAG 1574
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Claim 1; Page 204-205; 389pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABT07644 standard; cDNA; 386
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comprising: a sequence encoding a sequence comprising 11-1518 amino acids in a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 199-8144 at sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polymucleotides of the invention can be used to treat disorders by gene therapy. This polymucleotide represents a breast specific related sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1436 GGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAA 1495
                                                                                                                                                                                              New isolated nucleic acid molecule, useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAA
                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; gene therapy; colon cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 380.2; DB 8;
Pred. No. 2.3e-92;
n: Mismatches 3;
                                                                                                                  Pluta J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polynucleotide, SEQ ID NO: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1556 GTAATTCAACAGTTAAAAGAAGCTT 1580
                                                                                                                  Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 GTAATTCAACAGTTAAAAGAAGCTT
                                                                                                                                                                                                                                                                          Claim 1; Page 250; 377pp; English.
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21-NOV-2001; 2001WO-US043815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.2%;
                                    22-NOV-2000; 2000US-0252509P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.2
Best Local Similarity 99.2
Matches 382; Conservative
                                                                                                                  Macina RA,
                                                                           (DIAD-) DIADEXUS INC
                                                                                                                                                     WPI; 2003-018927/01.
                                                                                                                                                                                                                                     in a patient.
                                                                                                              Salceda S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer; metastatic; breast cancer; breast specific; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1196 AACCCCTGCCAGGCCCAGCTGCCACCCTTTCTGGGAGAAGGAGCCTACAGAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 CCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTTCACTGGGCCATGGGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                       Cafferkey R;
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                         Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breast specific related polynucleotide SEQ ID No 104
                                                       Karra K,
                                                                                                                                                                                                                                                                                                                                                                                                              cch 22.2%; Score 380.2; DB 6; al Similarity 99.2%; Pred. No. 2.3e-92; 382; Conservative 0; Mismatches 3;
                                                       Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1556 GTAATTCAACAGTTAAAAGAAGCTT 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a coding sequence of the invention
                                                                                                                                                                                                                                   Claim 1; Page 248; 367pp; English
                                                       Hu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABT13389 standard; DNA; 386
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                                                     Salceda S, Macina RA,
Sun Y, Liu C;
                DIADEXUS INC
                                                                                                              WPI; 2002-657582/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200277232-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                (DIAD-)
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Matches
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1315

61

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Gaps

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Indels

Length 386;

1375

121

181

1435

241

301

361

RESULT 11

us-09-989-890-105.rng

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The present sequence is one of 3351 sequences in a library of human polymucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polymucleotides me probes can be used for chromosome mapping of the polymucleotides of detection of transcription levels. Ribbzymes or antisense oligonucleotides can be generated. The polymucleotides and can be generated. The polymucleotides and blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and antibodies against them can be used in pharmaceutical compositions to treat the cancers and prollferative disorders such as neoplasia,
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321 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCATNCTTTCAGGGGCACCGACACAGACTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGCCCCGCCCTGGACACCCCCCCCCCAGCATCTGGGCCCTCCACGCTTGGGACCGTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; 88.
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arcia V, Jones LW, Strache-Crain B;
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20.3%; Score 347; DB 5; Length 42
Best Local Similarity 99.7%; Pred. No. 2.4e-83;
Matches 347; Conservative 0; Mismatches 1; Indels
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Kassam A, Reinhard C, Randazzo F, Kennedy GC,
Drmanac R, Crkenjakov R, Drmanac S, Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polynucleotide, SEQ ID NO: 2132.
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                                                                                                                                                                                                                                                                                                              AAF66376 standard; cDNA; 427 BP
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                                                                       1164 GTCGGGGCCACC 1175
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                                                                                                                                          381 Greededarce
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02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treat the cancers and proliferative disorders such as neoplasia,
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Pot D, Lam
Labat I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia PD, F
Kennedy GC, I
Dickson M,
       breast cancer; lung cancer; cancer detection; ss.
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Reinhard C, Randazzo F, Kennedy C
Crkenjakov R, Drmanac S, Dicksor
z D, Kita D, Garcia V, Jones LW,
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98.4%;
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99US-0142311P
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                                                                                                                                              WO200102568-A2
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02-JUL-1999;
                                                                          Homo sapiens
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                                                                                                                                                                                                                  11-JAN-2001.
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Drmanac R,
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Lamson G;

Klinger J; Pot D, La

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Length 427;

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CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCACGAGCCGC 120
                                                                              240
                                                                                         The present invention describes a library of human polynucleotides comprising the sequences given in AA212532 to AA217779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
                                                           TGGGTGTGGGGAGTGGTGCCGGGGCTGCTTCTGCTTCCGCCGCCTGCCGGGATTGCCTCCAG 300
                                                                                                                                  TGGGTGTGGGAGTGCCGGCCGCCTTCTGCTTCCGCCGCCGCGGATTGCCTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human genes and their expression products which are differentially expressed in different cell types.
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sitese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
nanac R, Cikvenjakov R, Dickson M, Drmanac S, Labat I;
Kita D, Garcia V, Jones WL, Stache-Crain B;
                                                                              ATCTCTGGCTGCTGCTGGCCGGCCCTTGAGTCCCCCCACCTGCTGCTGCTCTCGGCGACCC
                                        CGCACCCGTAGACCCAGAGCACCCTGGCCACCATGGGCCCAGAGATTACCTTC
                                                                                                                                                                                                                                                                                                             Human, gene, gene expression product, diagnosis, therapy, probe,
detection, mapping, tissue typing, profiling, forensic, cancer,
genetic analysis, colorectal cancer, breast cancer, lung cancer, ss.
                                                                                                                                                             CGCTGTGGAGCCTGTGTGCGGGATGCAGCCCCTGCCTGTCTACTGAG 348
                                                                                                                                                                       CGCTGTGGAGCCTGTGTGGGGGGGGGCCCCTGCCTGTCTACTGAG 427
                                                                                                                                                                                                                                                                                           Human gene expression product cDNA sequence SEQ ID NO:861.
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98US-0075954P.
98US-0080114P.
98US-0080515P.
98US-0080666P.
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24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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28-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     884
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polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis and management of colorectal cancer, breast cancer, peptide analogues and antagonists
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This invention describes novel isolated human polymucleotides obtained by screening for differential expression in colon cancer, breast cancer and lung cancer call lines. The polymucleotides of the invention are represented in AAX98275-X991B and encode polypeptides of protein families selected from 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbolesters or diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, cranscription factors, G-protein tyrosin, wut family of developmental signalling proteins and WM/rap5/WWW domain containing proteins. The corocated polypeptides also have a functional domain selected from Ank crepeat, basic region plus leucine zipper transcription factors, crepeat, cancers, mainlies and are predicted to have similar properties. The novel corocations in particular, the products for use as therapeutic agents and in forensics, genetic analysis, mapping and diagnostic applications. In particular, the product can be used for treating e.g. cervical cancers, melanomas, colorectal adenocarcinomas, wilm's tumour, sarcomas, retinoblastoma, myosarcomas, lung carcinomas, leukemia, and lymphomas such as histiocytic leukemia, and management of cancers. They can be used for treating e.g. cervical myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and lymphomas such as histiocytic leukemia, and hyperplasia, congenital alveolar dysplasia, and hyperplasias, e.g. endometrial, adrenal, breast, beast, be Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J; Standazzo F, Kennedy GC, Pot D, Kassam A; Hanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I; Kita D, Garcia V, Jones LW, Stache-Crain B; New isolated human polynucleotides. Claim 1; Page 326; 591pp; English. 98US-0105234P. 98US-0105877P. 98US-00217471. Leshkowitz D, Kita D, , Giese K, Drmanac R, WPI; 1999-430243/36. CORP. (CHIR ) CHIRON COR (HYSE-) HYSEQ INC. Williams LT, Reinhard C, 27-0CT-1998; 21-DEC-1998; 

Sequence 300 BP; 68 A; 90 C; 86 G; 56 T; 0 U; 0 Other;

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/product="hypochetical_start"
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Pred. No. 0;
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larity 92.9%;
Conservative
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Pan troglodytes FLJ34633 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. DQ045549 GI:66896764 GSSO.
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Pan troglodytes
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Hominidae, Pan.
1 (Basea I to 1181)
Nielsen, R., Bustamente, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
Mitte, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
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     AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 660
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.
Nielsen,R., Stledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
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                                                             GAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT
                                                                                                                                   GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC
                                                                                                                                                                                                                                                               AGCATCA CGCAGGACTACCACCTGGATGAGCAGGATGATGAGGGCCGCCTGGTACGCGGC
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                                                                                                                  GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC
                                                                                                                                                                                       AAGTGCACATCAGACACTGTGCTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC
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REFERENCE
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B. Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B. Whetbsz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans
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100.0%; Pred. No. 1.1e-296;
cive 0; Mismatches 0;
                                    A Scan for Positively Selected Gen
Chimpanzees
(er) PLoS Biol. 3 (6), E170 (2005)
15869325
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/db_xref="taxon:9606"
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/gene="FLJ34633"
/locus_tag="HC11301"
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshikayi,K., Yongawa,Y., Iranka,I., Matsuura,S., Watshiki,M., Yonacaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer [Genome Res. 10 (11), 1757-1771 (2000)
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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
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ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA
                                                            TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCCAGGAGACGACTGCAGATGCC
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Mus musculus 10 day old male pancreas CDNA, RIKEN Full-length enriched library, clone:181001916 product:SIMILAR TO TATA BOX BINDING PROTEIN (TPB)-ASSOCIATED FACTOR, RNA POLYMERASE II, Cl. 130KD homolog [Mus musculus], full insert sequence.
                                       ACTOGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC
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Nature 409, 685-690 (2001)
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Analysis of the mouse transcriptome based
of 60,770 full-length cDNAs
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High-efficiancy full-length CDNA
Meth. Enzymol. 303, 19-44 (1999)
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AK007551.1 GI:12841167
HTC; CAP trapper.
Mus musculus (house mouse)
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/mol_type="genomic DN
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/gene="FLJ34633"
/locus_tag="HC11301"
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                       CGCACCCGTAGACCAGGACCCTGGCCCACCATGGGCCAGAGAGCATTACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                      /codon start=1
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/brotein id="BAC25177.1"
/brotein id="BAC25177.1"
/dr xref="d1:26157449"
/translation="MARAPSPHRAVAPCGOTLRTLATTGORVSPSFQALQNQPTSPQPA
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PLASPPPTRALPSTFTNSPRGSTSFSFSFSDLDLPEWGSGSWSSRIDVLFFKCT
BLFSVHQIDBELAKCTSDTVFLBRTTSKISDLISSITQDYHLDBQDAEGRLVRGTIRIST
RKSRSRPQTSEGRSARSTAPAAAPDSGHETMLGSGLSQDELTVQISQSTADAIARKL
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                                                                                                                                                                                                    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (STREN) Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product; SIMILAR TO TATA BOX
BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE
II, Cl. 130KD homolog [Mus musculus] (SPTR|Q922Q0,
evidence: FASTY, 97.2%ID, 100%length, match=649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AGGCCATCAGAGTTATGCCTGGAAACGAAGGATGAGGGCTCCCAGCCCCACCAGGCCGT
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Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kabkawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M. Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K. Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C. Satich,H., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Suito,H., Salto,R., Shihata,X., Shihata,Y., Shihata,Y., Shihata,Y., Shihata,Y., Shihata,Y., Shihata,Y., Tajami,M., Tagawa,A., Shiraki,T., Sogab,Y., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,R., Tanaka,T., Yoshino,M., Muramatsu,M. and Hayashizaki,Y., Yoshida,K., Direct Submission
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Pred. No. 1.5e-233;
0; Mismatches 232; Indels
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/db_xref="taxon:10090"
/clone="1810019J16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="pancreas"
/clone_lib="RIKEN full-length
/dev_stage="10 day old"
138. 1241
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/strain="C57BL/6J"
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Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230011M17 product:hypothetical protein, full insert sequence.
AKO51860
AKO51860.1 GI:26342255
HTC: CAP trapper.
Mus musculus (house mouse)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                            ACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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E 1 (bases 1 to 975)

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Inth-MGC http://mgc.nci.nih.gov/.

Inth-MGC http://mgc.nci.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:

http://inage.lnl.gov

Plate: LLAM12141 row: f column: 07

High quality sequence stop: 659.

Location/qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs
Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

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E Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, D., Rukuda, S., Furuno, M., Haragaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hara, A., Haraka, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Konno, H., Konno, H., Kowai, M., Ohoa, M., Ohoato, N., Nakai, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Muramatsu, M. and Hayashizaki, Y., Towaru, A., Toya, T., Yasunishi, A.,
Direct Submission
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
                                                                                     new genes
                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Zakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new g
Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                                                                                                                                                                                                             Score 791; DB 4; Length 15
Pred. No. 3.8e-192;
0; Mismatches 145; Indels
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Best Local Similarity 85.8%;
Matches 891; Conservative
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745

548 865 608 925 668 985

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AGENCOURT 8341018 NIH_MGC_110 homo sapiens cDNA clone IMAGE:6249453 5', mRNA sequence. BQ691555.1 GI:21816871 EST.
                                                                                                          309 AGGAGCCACTGGCCGATCCCCCACCCAGCAGCAGCCTGCCCAGCACCTTTGCCAGTA 368
                                                                                                                                                                                           369 GTCCTCGTGGCTCCCGAGGAGTACTATTCTTTCCATGAGTCGGACCTGGACCTGCCGGAGA 428
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                       249 TCCCTGTGTATCCCTACCCGAGGCCACCTCCCCAGCCCCTGATGCGGACTCCTGCTGCA
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1 (bases 1 to 917)

NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: AFC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can by
ttp://image.llnl.gov
thtp://image.llnl.gov
oclumn: 22
High quality sequence stop: 535.
High quality sequence stop: 535.
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393 GCCGCTCTACTGCCC---CTGCTGCTGCCCCGACAGTGGCCATGAGACCATGGCGC 337
                                                                                                                                                                                                                                                                                                    EST 16-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGGAGCCTGTGTGCTGCGGGGATG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li-Y., XW.C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stancon, L.M.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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17000599935935 GRN_PREHEP Homo sapiens CDNA 5', mRNA sequence
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Fax: 650 473 760
Email: rbrandenbergeregeron.com
Insert Length: 753 Std Error: 0.00.
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Pred. No. 7.4e-177;
0; Mismatches 1;
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Regenerative Medicine
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1 (bases 1 to 753)
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ઠે d ò 셤 à g ઠે 셤 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.

EST. Mus musculus (house mouse) Mus musculus

BY707606.1

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/clone_lib="NIH MGC_IIO"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI, cDNA made by oligo-dr priming.
Site_2: EcoRI, cloned into EcoRI/XhoI sites using the following S' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Best Local Similarity 98.3
Matches 715; Conservative
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RESULT 9
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DEFINITION

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Scillogatani, murbicaes; murines; mus.

Scillogatani, murbicaes; murines; mus.

Scillogatani, murbicaes; murines; mus.

Nikaido, I., Osato, N., Saito, R., Suzuki, H.; Yamanakai.;

Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Maceuda, H.,

Batalov, S., Beisch, W., Blake, J.A., Bradt, D., Brusic, V.,

Rotchia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gaugh, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kurochkin, I.V., Lee, Y., Lehard, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lehard, B.L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Paran, W.J., Pertea, G., Pearole, C.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelinh, A., Schneider, C., Semple, C.A., Setou, M., Shultan, R., Takenaka, Y., Taylor, M., Shultan, R., Takenaka, Y., Taylor, M., Shultan, R., Wangers, C., Wunnhaw-Boris, A., Yanagiawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Kavazi, T., Yaun, Z., Savolan, M., Zhu, Y., Xanadi, J., Azawa, K.,

Sakazume, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawa, J., Azawa, K.,

Arakawa, T., Pukuda, S., Hara, A., Hashizume, W., Imotani, K.,

Shinagwa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Entucy, E., and Hayashizaki, Y.,

Analysis of the mouse transcriptome based on functional annotation of 60,770 cull-length Abashizayi.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence Lustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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BE741035 1015 bp mRNA linear EST 15-SEP-2000 601594018F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947861 5',
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution of distribution of distribution distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM810 row: d column: 06
                                                               840 CAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCG
                                                                                                  884 CAGCATCACGCAGGACTACCACCTGGATGAGCA-GACGCCGAGGGCCGCCTG--TGCGGG
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1 (bases 1 to 1015)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                              941 GATCATCCGTATTAGTATCGCAAAAGCTGCTCCGCCCACAGACTCCGAGGGGCGTC 996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3947861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 7
Location/Qualifiers
1. .1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              837; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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COMMENT
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 ATGCCCAGGCCGGGACAGCCCCGCCCATCATCTGGGCCTCCACGCTTGGGGCCCTGGGAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACATGGGCCAGAGAGCATTACCTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCACCAGGAGGCCAGACCCTAAGGACCCTGGCCACGGGCCAGGAGAGTATCACCTTC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTCAGGCTCTGCAGAACCAGCCAACGAGCCCCCAACCTGCTGCTCCTCTTGGCGCCCCC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 TGGGGTTGGGACTGGTGTAGGGCTGCCTTCTGCTTCCGACGCTGCAGGGATTGCCTGCAG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 AGGETCTGCCGAAGCCGCCTGGGCCAAGGAACACAATGGTGTGCCCCCCAGCCCAGACCG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 TGCACCCCCAGCCGCCGGGATGGCCAGAGGCTCAAGACAAGCATGGGCAGCAGCTTCAG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caderridectradeacetreaceaecaecececececerereagaracraerecerrica 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 704 TGAATCGGACCTGGACCTGCCTGAGATGGGCAGTGGCTCCATGTCGAGCCGGGAGATCGA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 CGTGCTTATTTTCAAGAAGCTGACAGAGCTGTTCAGCGTGCACCAGATTGACGAGCTGGC 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAG 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                              /tissue_type="pancreas"
/dev_stage="10 day old"
/clone_lib="RIKEN full-length enriched, 10 day old male
pancreas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 Aggiciarica a describar de conservados a describar de conservados de conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCCTTCCGCCGCTGCCGGGATTGCCTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 679.6; DB 5;
Pred. No. 1.7e-163;
                                                                                      'organism="Mus musculus"
                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="1810019J16"
                            Location/Qualifiers
                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.7%;
84.0%;
                                                                                                                                                                                                                                                  sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 803; Conservative
                                                               1. .1009
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cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM842 row: g column: 05
High quality sequence stop: 668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCACCTCAGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCCAAAGAACCCTGG-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCCGAGGAGTACTATTCTTTCCATGAGTCGGACCTGGACCTGCCGGAGATGGGCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.8%; Score 647; DB 2; Length 966; 93.9%; Pred. No. 4.2e-155; ive 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               750; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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1 (Abaes 1 to 966)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                               GGTGTGGGAGTGGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCG
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BP315176 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR07979, mRNA sequence.
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        GGGTACCCAGCAAGCCATGACTCATCCTTCCAGGGCACCGACCAGCACTCGTCGGGGGCCA
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        GGGTACCCAGCAAGCCATGACTCATCCTTCCAGGGCACCGACCAGCAAGCCTCGTCGGGGGCA
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1 (bases 1 to 582)

2 usuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
Block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

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Contact: Yutaka Suzuki
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                      61 GATGCTGAGGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCT
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GATGCTGAGGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCCGAAAGAGCCGTGCT
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yazuki@ins.u-tokyo.ac.jp.
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/clone="OFR07979"
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/cell type="Lymphoblast-like"
/cell line="SNU-16"
/lab_fost="DH10B"
/lab_fost="DH10B"
/clone lib="525XVI6n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_l: EcoRI;
Site_2: NotI; The $225XVI6 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                                                                                                                       622 bp mRNA linear EST 06-MAR-2002
K-EST0094733 S22SNU16n1 Homo sapiens CDNA clone S22SNU16n1-102-H01
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Vuseong-gu, Daejeon 305-333, South Korea
Tal: +82-42-860-4470
Fax: +82-42-860-4409
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100.0%; Pred. No. 1e-148;
tive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-102-H01"
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Plate: 102 row: H column: 01
High quality sequence stop: 622.
Location/Qualifiers
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Sciurognathi; Muroidea; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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                                                            Length 582;
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                                                           Score 577.8; DB 3;
Pred. No. 2.5e-137;
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/cell_line="OCUB-F"
/clone_lib="Sugano cDNA library,
/note="mammary gland tumor"
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Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAW1955 row: 1 column: 09
High quality sequence stop: 796.
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                                                                                                                                                                               /mol type="mRNA"
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/clone="IMAGE:5375384"
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Pred. No. 6.8e-137;
0; Mismatches 123;
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/organism="Mus musculus"
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Search completed: March 11, 2006, 22:01:33 Job time : 6313 secs
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                                                                                                                                                                         BP331524 Sugano cDNA library, rectum Homo sapiens cDNA clone RCT05504, mRNA sequence.
GGCTCAGGTCTCAGCCA--GGATGAGCTGACAGTGCAGATCTCCCCAGGAGACGACTGCAG 1075
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                 717 GGCTCTGGCCTCAGCCACGGACGGACTGACGTCCCAGATCTCCCAGGAGGACACAGGA 776
                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 58)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 TCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGCCGCACCCGTAGACCAGA 137
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                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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Corganisms=Homo sapiens"

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/db_xref="taxon:9606"

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/tisuse type="rectum"

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                                                               1076 ATGCCATCGCCCGGAAGCTGAGGCC 1100
                                                                                              777 GATGCATCGCCAGGAACTGAAGGC 801
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BP331524.1 GI:52260875
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                                                                                                                                                                                                                                             VERSION
KEYWORDS
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ORGANISM
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PUBMED
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                                                                                                                                                                                                                                                        481 CANAGGCATCCCTGTGTATCCCTACCCGNAGGCCANCTTCCCAGCNCCTGATGCGGACTC
CTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCG
                               361 CTGGGCCAAGGAGCACAATGGAGTGCCCCCCCAGCCCTGATCGTGCACCCCCCAGCGGGG
                                                                                                                                                                                                                        CAAAGGCATCCCTGTGTATCCCTACCCGAGGCCCACCTCCCCAGCCCCTGATGCGGACTC
                                                                                                                GGATGGCCAGCGCTCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGATGTTAAGCT
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270 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTCTCGCGGACCC 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 cecaccegradaccadaceceaaggacecragecacearggecaagagagagarracerre 269
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TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 799
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Best Local Similarity 99.9%;
Matches 1694; Conservative (
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; ORGANISM: Homo sapiens
US-10-104-047-799
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GENERAL INFORMATION:
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Sequence 153, App
Sequence 153, App
Sequence 6029, Ap
Sequence 6079, Ap
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Sequence 2, Appli
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                                                                                                                                                                                             March 11, 2006, 19:54:43; Search time 324 Seconds (without alignments) 9398.034 Million cell updates/sec
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202, A
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Sequence 16656, A
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Sequence 1429
Sequence 1429
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Sequence 17
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
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US-09-106-840A-2
US-09-016-434-1488
US-09-854-133-153
US-09-489-039A-6029
US-09-489-039A-6072
US-09-489-039A-6072
US-09-797-039-1
US-09-620-312D-19
US-09-620-312D-20
US-09-620-312D-20
US-09-620-312D-19
US-10-153-921-1
US-10-153-921-1
US-09-902-540-9140
US-09-902-540-9140
US-09-949-016-14290
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US-08-949-018-14291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                           US-09-989-890-105
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seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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Maximum DB 8
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Score 1692.8; Pred. No. 0; 0; Mismatches

DB 3; Length 1785; Indels 9

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υ	26	39	7.	2.3	۳	2207	σ	5221620-3	Patent No. 5221620
Q	27	39	7.	2.3	m	2656	m	US-09-902-540-295	Seguence 295, A
	28	38	œ.	2.3	ო	3004	m	US-09-991-181-112	_
	59	38	8.8	ς.	۳.	3004	m	US-09-990-444-112	112,
	30	38	۳.	2.3	٣	3004	٣	US-09-997-333-112	_
	31	38	₩.	2.3	m	3004	m	US-09-992-598-112	112,
	32	38	ω.	4	m	3136	٣	US-09-443-184-43	43, A
	33	38	ω.	ď	m	3136	m	US-09-806-536A-27	
U	34	38	9.	2.3	m	6043	m	US-09-949-016-2582	2583
υ	35	38	9.	ς,	m	6046	m	US-09-949-016-5830	5830,
O	36	38	9.	ς.		112219	m	US-09-949-016-12453	12453,
υ	37	38	9.	α,		112222	٣	US-09-949-016-14324	Sequence 14324,
υ	38	38	9.	ď		113186	٣	US-09-949-016-17572	Sequence 17572,
υ	39	38	9.	ď		4411529	m	US-09-103-840A-1	Sequence 1, Ap
	40	38	4.	2.2	~	3045	m	US-09-949-016-701	Sequence 701, App
	41	38	7	4	~	2677	m	US-09-949-016-1924	Sequence 1924,
	42	38	7	4	~	19237	m	US-09-949-016-13666	Sequence 13666,
υ	43		38	4	N	702	7	US-08-458-568A-3	
υ	44		38	۲,		12001	~	US-08-458-568A-11	H
	45		38	7	0	70308	ო	US-09-949-016-15601	
								ALIGNMENTS	
RESULT	ILT 1								
US-1	US-10-104-047-799	4-04	7-799	_				-10-104-047-799	

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556 GCCCTGAAGCAGCCTCCGGCGCCCCCTCCGCCACCCCCGCCAGTGTCGGCGCCCGCGGGCC 615
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                                                                                                                                                                                                                                                                                                                                   616 GAGGCCGCCCCCCCCCTCCGCCG 640
                                                                                                                                                                                                                                                                413 CTGATCGTGCACCCCCAGCCGGCG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 153, Application US/09370838
Parent No. 6444425
GENERAL INFORMATION:
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Patent No. 6759508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.4%;
Best Local Similarity 46.9%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapien
US-09-370-838-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-370-838-153/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 GCTGAGCTCCAGCTTCTTTGCCTCCCAGGGCTGCGCCCAGGAGTCCATTCCAGGCC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 GGGTGTGGGAAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGATTGCCTCCAGC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 - CACTGAGGGACTGCTGAAGCCAACTGGGCCCAAGGAGCACAATGGAGTGCCCCCCCAGCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 recadecrecrecedecedecedentes and reconstructores and recade --- destressed 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 GCTGCCGCCGTCGCTGCCGCGCCCCCGGCCCCTGCCGCCCTCTACGGTGGACACACAGCG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAGC
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
ITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
ITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42.2; DB 3; Length 1767;
Pred. No. 0.42;
0; Mismatches 218; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/016,434
FILLING DATE: HEREWITH
CLASSIFICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DALE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
""TRPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.5%;
Best Local Similarity 48.3%;
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CLONE: 9995934
US-09-016-434-1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
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179 TCATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGCTGGCGGC 238 764 TCTCCGCCGGCCCTGCTGTCTGGGGCCCCGGGCTCTCCCTCGGGGGCCACCTCCGGCCTG 705 239 CCTGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCC 298 584 CCGGGGCCGCCGCCGGGGGCCGTCCCCGTGCCCACTGGGGCTCGGCCCCCACTCCCGAGG 525 644 GGCGGCGGTGGCTGCGGCCTCGTGTTGTCTACCCATCCGGCCTTTGCGTCCACGCCCTT 585 Gaps ö APPLICANT: LOCATION Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT PILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0 Score 41.4; DB 3; Length 2109; Pred. No. 0.74; 0; Mismatches 146; Indels 0 APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadch
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
SEARLIER APPLICATION NUMBER: US 09/285,323
SEARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289 419 GTGCACCCCCCAGCCGGCGGGATGGCCAGCGGCTC 453 524 rccagccrcccagcccrrcccgccrcrccgccccc 490

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APPLICANT: Gary Ereton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
FRIOR APPLICATION NUMBER: US 60/117,747
FRIOR PLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6072, Application US/09489039A

Batent No. 6610836

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
GENY Breton et. al
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29
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2.4%; Score 40.8; DB 3; Length 465;
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TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
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JS-09-620-312D-19
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APPLICANT:
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332 CGGCGCTCGGCCTCGATGCCCTGACGTGCACGCCCGCCGGACCGTCATACCTATC 391
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; Sequence 3, Application US/09797039
; Patent No. 6730491
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6730491
GENERAL INFORMATION
APPLICANT: Clandt, Peter J.
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
TITLE OF INVENTION: KINABE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 10448-017001
CURRENT APPLICATION NUMBER: US/09/797,039
CURRENT PILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
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LENGTH: 1503
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US-09-797-039-3
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US-09-797-039-1
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TITLE OF INVENTION: Dolypeptides
TITLE OF INVENTION: Dolypeptides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/99/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_Genes Version 1.0
LENGTH: 2747
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2.4%; Score 40.4; DE
Best Local Similarity 53.9%; Pred. No. 1.4;
Matches 83; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2297
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                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: CDS
LOCATION: (154)...(1656)
NAME/KEY: misc_feature
LOCATION: (1)...(2297)
CTHER INFORMATION: n = A,T,C or G
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asund, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Ping-Rui

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; LOCATION: (206)..(1618)
US-09-620-312D-19
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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528 TIGACIGGAICCIGGACCAGGGCIACTACICGGA 561
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                                                                                                            408 AGAACGAGGATCCTCAAGATGGTGAAGCATCCCAACATCCTACAGCTGGTGGATG 467
                                                                                                                                                 773 AGCTGGCCAAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACC 832
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                                        Gaps
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2.4%; Score 40.4; DB 3; Length 2747; 53.9%; Pred. No. 1.5;
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                                    71; Indels
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APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: Dramac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/05/620,312D
CURRENT FILING DATE: 2000-07-19
FILOR PEDICATION NUMBER: 09/552,317
PRIOR PEDICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 100-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NOS: 1105
SEQ ID NO 20
LENGTH: 2840
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                                    0; Mismatches
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Pred. No. 1.
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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
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Best Local Similarity 53.9
Matches 83; Conservative
                                    83; Conservative
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Wehrman, Tom
Xue, Aidong J.
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; LOCATION: (206)..(1711)
US-09-620-312D-20
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ORGANISM: Homo sapiens
                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-620-312D-20
 Query Match
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APPLICANT:
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                                    Matches
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Sequence 1, Application US/10153921

Sequence 1, Application US/10153921

Sequence 1, Application US/10153921

Setent No. 6653116

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO00612D1V

CURRENT APPLICATION NUMBER: US/10/153,921

CURRENT PILING DATE: 2002-05-24

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PASESEQ for Windows Version 4.0

LENGTHRENTH: 3124
                                      Sequence 1, Application US/09734030

Sequence 1, Application US/09734030

Patent No. 6461846

GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M.
APPLICANT: WEI, Ming-Hui
APPLICANT: WIL, Ming-Hui
APPLICANT: YAP CHUNNA
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
CURRENT PEPLICATION NUMBER: US/09/734,030

CURRENT FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 AGAACGAGATAGGCATCCTCAAGATGGTGAAGCATCCCAACATCCTACAGGTGGATG 472
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Pred. No. 1.6;
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53.9%; Pred. No. 1.6;
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0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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ORGANISM: HOMO SAPIEN
US-10-153-921-1
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Best Local Similarity
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Matches 83; Conserv
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ORGANISM: HUMAN
RESULT 13
US-09-734-030-1
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0; Gaps

71; Indels

0; Mismatches

83; Conservative

Matches

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Sequence 1. Application US/10669689
| Patent No. 680471
| GENERAL INFORMATION:
| APPLICANTY YAN, Chunhua et al.
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: CLO00612DIVII
| CURRENT APPLICATION NUMBER: US/10/669,689
| CURRENT FILING DATE: 2003-03-25
| PRIOR PELING DATE: 2000-12-12
| PRIOR PELING DATE: 2000-12-12
| PRIOR FILING DATE: 2000-05-30
| NUMBER OF SEQ ID NOS: 3
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 1
| LENGTH: 3124
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                                 413 AGAACGAGATAGGCATCCTCAAGATGATGAGCATCCCAACACCTACAGCTGGTGGATG 472
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ORGANISM: Homo sapiens
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/ cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
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/ cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1705, Ap 34, Appl 34, Appl 116, Appl 973, App 10967, A 6792, Ap 44, Appl 144, Appl Sequence 105, App Sequence 799, App Sequence 56, Appl 3497, Description Sequence 1 Sequence 1 Sequence 5 Sequence 1 Sequence 5 Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence S Sequence Sequence Sequence Sequence Sequence US-09-989-800-105
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US-00-989-920-56
US-00-989-920-117
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US-10-779-543-10096
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US-10-779-543-144
US-10-029-899-973
US-10-029-899-973
US-10-029-86-10967
US-10-029-86-10967
US-10-029-1448-44
US-10-723-860-3497 SUMMARIES Query Match Length DB 120 2761 513 1242 2359 2370 1412 1767 1692.8 1602.4 602.4 603.6 603.6 380.2 380.2 350.2 350.2 347 300 298.4 46.4 45.6 45.6 42.8 42.2 42.2 Score 120 9 11 11 14 14 Result υυ

Sequence 7, Appli Sequence 1181, Ap Sequence 1189, A Sequence 1952, Ap Sequence 7952, Ap Sequence 12031, Sequence 153, App Sequence 153, App Sequence 153, App Sequence 153, App	Sequence 48, Appl Sequence 48, Appl Sequence 487, Appl Sequence 10204, Appl Sequence 10204, Appl Sequence 120327, Sequence 120327, Sequence 12, Appl Sequence 6, Appl Sequence 6, Appl
US-10-761-169-7 US-10-087-192-1181 US-10-029-386-17895 US-10-029-386-4195 US-10-450-763-7952 US-10-450-763-7951 US-09-738-973-153 US-09-738-973-153 US-09-854-133-153 US-10-1450-763-28779	US-10-288-798-48 US-10-362-892-48 US-09-764-891-5477 US-09-764-891-10204 US-10-205-428-11031 US-10-450-763-3762 US-10-450-763-3762 US-10-329-079-12 US-11-329-079-6 US-11-329-079-6
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## ALIGNMENTS

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Page 2

Db 1321 TGCCTTGGCTCCCAGCTGTCCTGCATTTCACTGGGCCATGGGATCTACATC 1380  Qy 1381 TCCTTGCATCCCCAGCTGTCTGATCCCTGCCAGGGCCCTTCCTT	RESULT 2 US-10-104-047-799 ; Sequence 799, Application US/10104047 ; Publication No. US20030236392A1 ; GENERAL INFORMATION: ; APPLICANT: HELLIX RESEARCH INSTITUTE ; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA ; FILE REFERENCE: H1-A0105 ; CURRENT APPLICATION NUMBER: US/10/104,047 ; CURRENT PILING DATE: ; PRIOR PILING DATE: ; PRIOR PILING DATE: ; PRIOR PILING DATE: ; SEQ ID NOS: 4096 ; SOFFWARE: Patentin Ver. 2.1 ; SEQ ID NO 799 ; LENGTH: 1785 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-104-047-799	Query Match         98.8%; Score 1692.8; DB 6; Length 1785;           Best Local Similarity 99.9%; Pred. No. 0;         0; Mismatches 2; Indels 0; Gaps 0;           QY         1 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCCTCCAGCTTGGGACCGTGGGAG 149           QY         4 ATGCCCGCCCTGGACACACATCTGGGCCTCCAGCTTGGGACCGTGGGAG 149           Db         90 ATGCCCGCCTGGACACATCTGGACATATGATAAACCACCTCAGCCCCACCAGCGCG 149           QY         61 CGGCCAACAGGACTATGATAAAACCACCTCAGCCCCCACCAGCGCG 209           Db         150 CGGCCAACAGGACTATGATAAAACACCACCCCACCAGAGACCCCCACCAGCGCCCCACCA
	661 GAGTCGGACCTGGCGGAGATGGGCACTCCATGTCGAGCCGAGAAATTGAT 720 661 GAGTCGGACCTGGCCGGAGATGGGCACTCCATGTCGAGCCGAGAAATTGAT 720 661 GAGTCGGACCTGCACGAGATGGCATGGCTCCATGTCGAGAGAAATTGAT 720 721 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACCCAGATCGATGGCTGGC	

	RESULT 4  US-09-989-920-117  i Sequence 117, Application US/09989920  i Sequence 117, Application US/09989920  i Sequence 117, Application US/09989920  i Retent No. US20020172957A1  i GENERAL INFORMATION:  i APPLICANT: Recipon, Herve  i APPLICANT: Chen, Sei-Yu  i APPLICANT: Liu, Chenghua  i APPLICANT: Liu, Chenghua  i TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes  i TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes  i TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes  i TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes  i CURRENT FILING DATE: 2001-11-21  i PRIOR APPLICATION NUMBER: 60/252,500  i WUMBER OF SEQ ID NOS: 284  i SOFTWARE: PatentIn Version 3.1  i ENGTHARE: DATE  i CRAMISM: Homo sapien  US-09-989-920-117	Query Match         93.5%;         Score 1602.4;         DB 3;         Length 1977;           Best Local Similarity         99.0%;         Pred. No. 0;         Antiches 1707;         Conservative 0;         Mismatches 6;         Indels 11;         Gaps 9           Qy         1 ATGCCCGGCCTGGACACCCCGGCCAGCATCTGGGCCTTGGGACCGTGGGAG 60	Oy 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAACCACCACCACCACCACCACCACCACCACCACCACCA	0. 4. U. R	Qy 300 GCGTGTGGA-GCCTGTGCGGGGATGAGCCCTGCCTGTCTACTGAGGACT-CCACT 357
0y         35B         GAGGGACTGCTGAAGCCAACTGG-GCCAAGGACCACAATGGAGTGCCCCCCAGCCCTGA         416           11	11	Qy         1010         CCATGGTGGGCTCAGGTCTCAGCCAGGATGACAGTCTCCCCAGGAGACGA         1069           Db         1274         CCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCCAGGAGACGA         1333           Qy         1070         CTGCAGATGCCATCGCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCC         1129           Db         1334         CTGCAGATGCCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCCAGGGTACCCAGCAAGCC         1393	OY 1130 ATGACTCATCCAGGGCACCGACAGACTCGTCGGGGGCACCCTTGCTCCAGGTGT 1189	AATGAAGAGGGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGAATGAACTAGAACTGAAGCAGTGCAATGAATG	Qy 1370 GGATCTACATCTCGCAGCTGGTCTGATCCCTGCCAGGCCCCTTCCTT

Genes and Prote

	RESULT 5  US-10-074-475-124  i Sequence 124, Application US/10074475  sequence 124, Application US/10074475  sequence 124, Application No. US2003009289&1  i GENERAL INFORMATION:  APPLICANT: Salceda, Susana  APPLICANT: Hu, Fing  APPLICANT: Karra, Kalpana  APPLICANT: Cafferkey, Robert  APPLICANT: Uiu, Chenghua  ITTLE OF INVENTION: Compositions and Methods Relating to Breast Specific  ITTLE OF INVENTION: Genes and Proteins  FILE REFERENCE: DEX-03.3  CURRENT APPLICATION NUMBER: US/10/074,475  CURRENT APPLICATION NUMBER: G0/268,292  PRIOR FILING DATE: 2001-02-13  FRIOR FILING DATE: 2001-02-13  FRIOR FILING DATE: 2001-02-13  NUMBER OF SEQ ID NOS: 295  SOFTWARE: PatentIn version 3.1  SEQ ID NO 124  LENGTH: 654  TYPE: DNA  CREANISM: Homo sapien  US-10-074-475-124	Owery Match         35.5%; Score 607.6; DB 5; Length 654;           Best Local Similarity         96.6%; Pred. No. 5.1e-178;           Matches 632; Conservative 0; Mismatches 19; Indels 3; Gaps 1;           QY         89 ArgaranaCcaccacaccacaccacaccacaccacaccacacc
358 GAGGGACTGCTGAAGCCAACTGG-GCCAAGGAGCACAATGGAGTGCCCCCAGCCCTGA 416 [		1070 CTGCAGATGCCATCGCCCGGAAGCTGATGCAGCTTCCAGGCTACCCAGCAAGC 1129  11310 ATGACTCATCCTTCCAGGCCCCACACACACACACCTTATGGAGCTCCAGGCTACCCAGCAAGC 11393  1130 ATGACTCATCCTTCCAGGCCCACACACACACACACCCTTCTGGAGCACCCTTGCTCCAGGTGT 1189  1130 ATGACTCATCCTTCCAGGCCCAGCACACACACACACACCCTTGCTCCAGGTGT 1183  11454 ATGACTCATCCTTCCAGGGCCCAGCACCCACACCCTTTCTGGAGAGCATGGCCTACAG 1249  1150 ATGACTCAACCCTGCCAGGCCCAGCACCCACACCTTTCTGGAGAGCATGGCCTACAG 1213  1250 AATGAAGAGGGGCCAGGCCCACACCCTTTCTGGAGAGCATGGCCTACAG 1513  12514 AATGAAGAGGGGCCAGGAACCCTGTGGGAGAGCATTCAGAGCCACT 1309  11515 AATGAAGAGGGGCCCAGGAACCCTGTGGGAGAGCATTCACTGGGCCACT 1573  1310 CTGGCTCCTCGCTTGCTGACTCCTGGACACATGTGCATTTCACTGGGCCATG 153  1370 GGATCTACATCTCCTTGCATCCCCAGGACCATGTGCATTTCACTGGGCCATG 1633  1370 GGATCTACATCTCCTTGCATCCCCAGGTGCTTCCTTCCT 1429  11430 GCTCATGGTTCCTTGCATCCCCAGGTGGTCTGATCCTTCCT

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Query Match 27.0
Best Local Similarity 88.4
Matches 569; Conservative
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Publication No. US20050227917A1

Sequence 5731, Application US/10779543

Publication No. US20050227917A1

Sequence 5731, Application US/107791

Publication No. US20050227917A1

APPLICAMY: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIPPERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REPERENCE: 2300-21302

CURRENT APPLICATION NUMBER: US/10/779,543

PRIOR PILING DATE: 1998-12-21

PRIOR PELING DATE: 1998-12-23

PRIOR PELING DATE: 1998-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR PLING DATE: 1998-10-21

PRIOR PLING DATE: 1998-10-21

PRIOR PLING DATE: 1998-10-21

PRIOR PLING DATE: 1998-01-28

PRIOR FILING DATE: 1998-01-38

                                                         447 -GCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGATGTTAAGCTCAAAGGCA
                                                                                            361 CGGGCTGCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGGATGTTAAGCTCAAAGGCA
                                                                                                                                                                                                                                            566 AGGAGCCACTGGCCGATCCCCCACCCATGCGACACAGCCTGCCCAGCACCTTTGCCAGTA
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LOCATION: 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 20,

LOCATION: 22, 23, 24, 25, 28, 29, 30, 36, 41, 85, 89, 97, 106, 108,

LOCATION: 115, 134, 139, 177, 185, 207, 232, 275, 283, 303, 320, 327,

LOCATION: 356, 414, 411, 469, 551, 566, 582, 588, 591, 605, 631, 656

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5731
                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGCAGTGCCTCCATGTCGAGCCGAGAAATTGATGTGCTCATCTTCAAGAAGC
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NAME: MARGYKEX: misc feature
LOCATION: 661, 678, 681, 687, 689, 702, 706, 710, 711, 713,
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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US-10-779-543-5731
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sel-Yu
APPLICANT: Chen, Sel-Yu
APPLICANT: Chen, Sel-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO 55
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapien
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Length 728;
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     DB 9;
     27.0%; Score 463.2; DB 9;
88.4%; Pred. No. 4.6e-133;
iive 0; Mismatches 66;
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APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
TITLE OF INVENTION: Genes and Proteins
TITLE OF INVENTION: Capositions and Proteins
TITLE OF INVENTION: Capositions and Proteins
TITLE OF INVENTION: Caposition and Proteins
TITLE OF INVENTION: Caposition Caposition and Methods Relating to Breast Specific
TITLE OF INVENTION: Caposition and Methods Relating to Breast Specific
TITLE OF INVENTION: Caposition and Methods Relating to Breast Specific
TITLE OF INVENTION: Caposition and Methods Relating to Breast Specific
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TITLE OF INVENTION: Caposition and Methods Relating to Breast Specific
TITLE OF INVENTION: Caposition and Methods Relating to Breast Specific
TITLE OF INVENTION: Caposition and Methods Relating to Breast Specific
TITLE OF INVENTION: Caposition and Methods Relating to Breast Specific Application and Methods Relating to Breast Specific App
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99.2%; Pred. No. 2.5e-107;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 123, Application US/10074475; Publication No. US20030092898A1
GENERAL INFORMATION: APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.2
Matches 382; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-074-475-123
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Publication No. US20040166105A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Pluca, Jason
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and ITLE REFERENCE: DEX. 20207-11-21
CURRENT APPLICATION NUMBER: US/09/989,890
CURRENT FILING DATE: 2001-11-21
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                                                                                                                                                                         1190 ACTGCTAACCCCTGCCAGGCCCAGCTGCCACCTTTCTGGGAGAAGCATGGCCTACAG 1249
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                                                                DB 3; Length 385
                                                                                                                  0; Indels
                                                          22.5%; Score 385; DB 3;
100.0%; Pred. No. 8e-109;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/252,509
PRIOR FILING DATE: 2000-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin version 3.1
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Best Local Similarity 99.2
Matches 382; Conservative
                                                                                       Best Local Similarity 100.
Matches 385; Conservative
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ORGANISM: Homo sapien
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US-09-989-890-104
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        US-09-989-920-55
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LENGTH: 386
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1105 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCCTTCCA-GGGCACCGACACAGACTC 1163
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                                                                                                                                                 321 GGAGCTCCAGGGTACCCAGGAAGCCATGACTCATTCTTTCAGGGGCACCGACCAGACTC 380
   261 ACAGTGCAGATCTCCCAGGACACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTAT 320
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US-10-779-543-12031
Sequence 12051
Publication No. US2005022791741
GENERAL INFORMATION:
APPLICAMY: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: UN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT APPLICATION NUMBER: US/10/779,543
FILE REPERIOR DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 09/217,471
PRIOR FILING DATE: 1991-12-21
PRIOR PRILING DATE: 1997-12-23
PRIOR PELING DATE: 1998-12-21
PRIOR PELING DATE: 1998-12-21
PRIOR PELING DATE: 1998-04-03
PRIOR PELING DATE: 1998-04-03
PRIOR PELING DATE: 1998-04-03
PRIOR PELING DATE: 1999-04-03
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1999-04-38
PRIOR PELING DATE: 1999-03-31
PRIOR PELING DATE: 1900-03-31
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Pred. No. 5.6e-97;
0; Mismatches 1; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-12051
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Best Local Similarity 99.7%;
Matches 347; Conservative
                                                                                                                                                                                                                                     1164 GTCGGGGGCACC 1175
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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302 CCCTGACTCCATCCCCTATTGCCACCCTAACCATCATGCAAACTTCTCCCTGGG 361
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NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10096
LENGTH: 393
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TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF US
FILE REFERENCE: 2300-21302
CURRENT FILING DATE: 2002-02-12
PRIOR PILICATION NUMBER: US/10/76,555
PRIOR PLICATION NUMBER: 09/217,471
PRIOR PLILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-10-31
PRIOR PELICATION NUMBER: 60/080,664
PRIOR PELICATION NUMBER: 60/105,234
PRIOR PELICATION NUMBER: 60/105,234
PRIOR PELING DATE: 1998-04-03
PRIOR PELING DATE: 1998-04-03
PRIOR PELING DATE: 1998-01-02
PRIOR PELING DATE: 1998-01-04
PRIOR PELING DATE: 1998-01-28
PRIOR PELING DATE: 1998-01-24
PRIOR PELING DATE: 1998-01-34
PRIOR PELING DATE: 1998-01-34
PRIOR PELING DATE: 1998-01-34
PRIOR PELING DATE: 1998-01-34
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Pred. No. 9.8e-99;
0; Mismatches 5;
                                                                                                     1556 GTAATTCAACAGTTAAAAGAAGCTT 1580
                                                                                                                                          362 GTAATTCAACAGTTAAAAGAAGCTT 386
                                                                                                                                                                                                                                                                                                                             Sequence 10096, Application US/10779543
Publication No. US20050227917A1
GENERAL INFORMATION:
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; LCCATION: 355
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-10096
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Best Local Similarity 98.4%;
Matches 366; Conservative
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ORGANISM: Homo sapiens
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241 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCCAGGTACCCAGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
ITILE OF INVENTION: Novel Human Genes and Gene Expression
TITLE OF INVENTION: Products I
FILE REBERRENCE: 2300-1480
CURRENT APPLICATION NUMBER: US/10/076,555
CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/217,471
PRIOR PELLING DATE: EARLIER FILING DATE: 1998-12-21
PRIOR PILING DATE: EARLIER FILING DATE: 1998-12-23
PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-27
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-27
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 300;
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                                                                                                                                                                                                                                                                                                          APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Garcia, Pablo Dominiguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
                                                                                                                                                                                                         Sequence 34, Application US/10076555 Publication No. US20030065156A1 GENERAL INFORMATION:
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Dickson, Mark
Drmanac, Snezana
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Kennedy, Giulia C.
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Leshkowitz, Dena
Kita, David
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Lamson, George
Drmanac, Radoje
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pot, David
                                                                                                                                                                        US-10-076-555-34
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                                                                                                                                                   320 TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCGCCCGCTGCCGGGATTGCCTCCAG 379
                                                                                                        TCCGCCGCTGCCGGGATTGCCTCCAG 300
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US-1U-179-543-1705

Sequence 1705, Application US/10779543

Publication No. US20050227917A1

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REFERENCE: 2300-212

PRIOR PLICATION NUMBER: 10/076,555

PRIOR PLING DATE: 1990-12-21

PRIOR PLING DATE: 1999-12-21

PRIOR PLING DATE: 1999-12-21

PRIOR PLING DATE: 1999-12-21

PRIOR PLING DATE: 1999-12-23

PRIOR PLING DATE: 1998-10-21

PRIOR PLING DATE: 1998-04-03

PRIOR FILING DATE: 1998-00-128

PRIOR FILING DATE: 1998-10-21

PRIOR PLING DATE: 1998-10-21

PRIOR PLING DATE: 1998-10-21

PRIOR PLING DATE: 1998-10-21

PRIOR PLING DATE: 1998-00-128

PRIOR PLING DATE: 1998-01-28

PRIOR PLING DATE: 1998-01-38

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                                                                                                                                                                                                                                                                             DB 9; Length 300;
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100.0%; Pred. No. 2.1e-82;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               10-779-543-1705
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LENGTH: 300
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Search completed: March 11, 2006, 22:42:56 Job time : 1289 secs
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980 CCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGCTCAGGTCTCAGGCCAGGATG 1039
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| Sequence 34, Application US/10779543
| Publication No. US20050227917A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TILLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
| TILLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
| FILE REFERENCE: 2300-21302
| CURRENT APPLICATION NUMBER: US/10/779,543
| CURRENT FILING DATE: 2004-02-12
| PRIOR FILING DATE: 1998-12-21
| PRIOR FILING DATE: 1998-10-23
| PRIOR FILING DATE: 1998-10-21
| PRIOR FILING DATE: 1998-01-28
| PRIOR PRIOR APPLICATION NUMBER: 60/080,114
| PRIOR FILING DATE: 1998-01-28
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NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-989-920-116/c
                                                                                                                                                                   RESULT 14
US-10-779-543-34
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LENGTH: 300
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; Sequence 116, Application US/0998920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Yongming
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT FILING DATE: 2001-11-21
; CURRENT FILING DATE: 2001-11-22
; PRIOR APPLICATION NUMBER: 60/252,500
; FRIOR TILING DATE: 2001-11-22
; NUMBER OF SEG ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; TENGRA 20116
; TENGRA 20116
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100.0%; Pred. No. 1.6e-26;
tive 0; Mismatches 0;
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Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-116
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Query Match
98.8%; Score 1692.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches
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APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/11/072,512 CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR PLILAGION NUMBER: UP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 799, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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SEQ ID NO 799
LENGTH: 1785
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NAGAI, KEIICHI
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GRGANISM: Homo sapiens
US-11-072-512-799
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                                                                                                                                           March 11, 2006, 20:00:54; Search time 591 Seconds (without alignments) 6687.647 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2 US-11-036-568A-22110

US-11-096-568A-22110

US-10-330-773-603

US-10-522-037-2

US-09-925-065A-551694

US-09-925-065A-52104

US-09-925-065A-52109

US-09-925-065A-521094

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US-09-925-065A-56292
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 13469, A Sequence 13296, A Sequence 2907, Ap Sequence 73, Appl Sequence 73, Appl Sequence 13177, A Sequence 55078, A Sequence 55078, A Sequence 55078, A Sequence 55078, A Sequence 55177, A Sequence 54937, A Sequence 24937, A Sequence 6485, App
B US-10-995-561-13469 B US-10-995-561-13296 12 US-11-124-36RA-2907 US-00-925-065A-732133 7 US-10-921-793-73 7 US-10-931-138-73 8 US-10-95-561-13376 8 US-10-750-185-31877 8 US-10-750-185-31877 8 US-10-750-185-31877 8 US-10-750-185-35078 9 US-11-072-512-977 US-11-072-512-977 US-11-072-512-977 US-11-072-512-977 US-11-072-512-977 US-11-072-512-977 US-10-330-773-159 US-10-330-773-159 US-10-330-773-25 US-10-330-773-25 US-10-330-773-25 US-10-350-058-56117 US-10-350-058-56117 US-10-350-058-56117 US-10-350-058-9317 US-10-750-185-24937 US-10-750-185-24937 US-10-730-131-826A-485
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DB 9; Length 1785; Indels ~

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Sequence 144, Application US/10501035

Publication No. US20060046249A1

Publication No. US20060046249A1

Publication No. US20060046249A1

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING

TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS

FILE REPERENCE: D0185 PCT

CURRENT APPLICATION NUMBER: US 10/501,035

CURRENT FILING DATE: 2004-07-09

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 795

SOPTWARE: Patentin version 3.2

SEQ ID NO 144
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1710 CTATGTTATGTTAAGGAGTTGGTTCTTGGTTCTTGGCTGATGTTCTGTATCTTAACATGAC 1769
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creccaseccasergecacecrrrrerssaaaaaacarssecraeaaarsaaases
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48.1%; Pred. No. 0.76;
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ORGANISM: Homo
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US-10-501-035-144
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Sequence 155, Application US/11124368A
; Sequence 155, Application No. US20050287559A1
; Sequence 155, Application No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Wichele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vaccular Diseases, Methods of Detection and Uses Thereof
; TITLE OF INVENTION: Vaccular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR FILING DATE: 2004-11-09
; PRIOR PLING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTHARE: PRESENCE for Windows Version 4.0
; SEQ ID NO 155
LENTH: 3.422
                                                                                                                                                                                                                                                                                       APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: Machele Cargill
APPLICANT: My Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: VASCULAR DISEASE
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 155
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US-11-124-368A-156
; Sequence 156, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-124-368A-156
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Publication No. US20050287559A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Maichel Cargill
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION WUBSER: US 60/568,845
CURRENT APPLICATION WUBSER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FRELSEQ for Windows Version 4.0
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Best Local Similarity 53.99
Matches 83; Conservative
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CORGANISM: Homo sapiens
US-11-124-368A-154
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US-11-124-368A-154
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LENGTH: 3320
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GCACCAGGA 1269
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US-09-925-065A-894029
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AGCTGGCCAAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACC 832
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APPLICANT: Wang, David G.
ITILE OF INVENTION: Identification and Mapping of Single; TITLE OF INVENTION: Identification and Mapping of Single; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome; TITLE OF INVENTION NUMBER: US/09/925,065A; US/07RENT PELING DATE: 2001-00-80 PRIOR FILING DATE: 2000-10-24; PRIOR FILING DATE: 2000-11-20; PRIOR FILING DATE: 2000-11-30; PRIOR FILING DATE: 2001-01-16; PRIOR PRIOR DATE: 2001-01-16; PRIOR APPLICATION NUMBER: US 60/261,766; PRIOR APPLICATION NUMBER: US 60/289,846; PR
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Publication No. US20040181048A1
GENERAL INFORMATION
GENERAL INFORMATION: US20040181048A1
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
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Pred. No. 1.9;
0; Mismatches
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Conservative
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Best Local Similarity
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US-09-925-065A-894029/c
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Sequence 519, Application US/11052554A

Sequence 519, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:

APPLICATION Schdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: UN 173/DEL/2004

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR PILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PatentIn version 3.3

SEQ ID NO 519

LENGTH: 5706
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50.3%; Pred. No. 1.9;
iive 0; Mismatches 94; Indels
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Pred. No. 3.8;
0; Mismatches 119;
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASESEQ FOr Windows Version 4.0
SEQ ID NO 894029
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Best Local Similarity 48.0%;
Matches 110; Conservative
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Matches 95; Conservative
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                                                           11 CTGGACACCCCCCCCCCAGCATCTGGGCCTTCCACGCTTGGGACCGTGGGAGCGGCCAACAG
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; Sequence 603, Application US/10330773
; Publication No. US20060040262A1
; GABERAL INFORMATION:
APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 603
; LENGTH 38239
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ilarity 43.3%; Pred. No. 4.7;
Conservative 0; Mismatches 229; Indels
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Best Local Similarity 50.0%; Pred. No. 13;
Matches 94; Conservative 0; Mismatches 94;
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Best Local Similarity
Matches 175; Conserv
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US-10-330-773-603
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APPLICANT: Worth
APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 306
LENGTH: 15234
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                                                                                                     1927 eccecceccaaeccerreccerriceaaaacceccicrecce 4879
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                                                              283 TGCCGGGATTGCCTCCAGCGCTGTGGAGCCTGTGTGCGGGATGCAGCC 331
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Pred. No. 8.6;
0; Mismatches 107; Indels
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LOCATION: (1). (1). (1431)
OTHER INFORMATION: Ceres Seq. ID no. 12407603
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                                                                                                                                                                                                           Sequence 306, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
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; ORGANISM: Rattus norvegicus
US-11-136-527-306
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Matches 102; Conservative
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US-11-096-568A-22110/c
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                                                                                                                                                                        RESULT 9
US-11-136-527-306/c
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: UNCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
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Pred. No. 5.5;
1; Mismatches 144; Indels
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 72
LENGTH: 162173
                                                                                                                                        Query Match 2.2%;
Best Local Similarity 47.9%;
Matches 136; Conservative
; LENGTH: 1067
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-551694
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                       Sequence 2, Application US/10522037

Sequence 2, Application No. US20050282166A1

GENERAL INFORMATION:

APPLICANT: LIBRAGEN

TITLE OF INVENTION: Method for the expression of unknown environmental DNA into adapt

TITLE OF INVENTION: cells.

FILE REFERENCE: B0149W0

CURRENT APPLICATION NUMBER: US/10/522,037

CURRENT PILING DATE: 2005-01-24

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827, 135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: DNA sequence of clone FS3-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 551694, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial sequence
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US-09-925-065A-551694/c
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                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
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5748 GCCCAGAAGCACGTTGGCAACATGGTGAGGCTGCCCAGTGTTCAGCGCAAAG 5696
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; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER: OF SEQ ID NOS: 795
; SQOFTWARE: PatentIn version 3.2
; SQO ID NO 200
LENGTH: 6034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-501-035-200
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      GTCTGGAGACATATGATAAACCACCTCAGCCCCCCAAAGCCGCCGCACCCGTAGACCAG
                           GTCTGGAGAGACATATGATAAAACCACCTAGCCCCCACCAAGCCGCCGCCGCACCCGTAGACCAG
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                                                                                   ACCCCAAGGACCCTGGCCACCACCAGGGCCAGAGAGCATTACCTTCATCTCTGGCTCTGCTG
                                                                                                                                                                197 AGCCGGCCCTTGAGTCCCCCACCTGCTGCCTGCTCTGGCGACCCTGGGTGTGGGAGTGGT
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YPASHDSSFQGTDTDSSGAPLLQVYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Info@bcgsc.bc.ca Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babbkaiff, Dave Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.W., Jones, S.J. and Marra, M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bathesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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through the I.M.A.G.B. Consortium/Linkl at: http://image.llnl.gov
Series: IRAL plate: 43 Row: c Column: 17.
Location/Qualifiers
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/clone="MGC:45763 IMAGE:3960220"
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/clone lib="NHH MGC 21"
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/protein id="AAH33143.1"
/db_xref="G1:21619959"
/db_xref="GeneID:126694"
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100.0%; Pred. No. 0;
ive 0; Mismatches
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/gene="Clorf172"
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Best Local Similarity 100.
Matches 1620; Conservative
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TITLE
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PUBMED
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AUTHORS
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Db 150 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCG	OY 121 CGCACCCGTAGACCACCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC	Oy 181 ATCTCTGGCTCTGAGCCGCCCTTGAGTCCCCCACCTGCTGCCTGC	Ay 241 TGGGTGTGGGAGTGGTGCCGGCTGCCTTCTGCTTCCGCCGCTGCCGGATTGCCTCCAG	Qy 301 CGCTGTGGAGCCTGTGTGCGGGATGCCAGCCCTGCCTGTCTACTGAGGACTCCACTGAG	Qy 361 GGGACTGCTGAACTGGGCCAACTGGGCCAATGGAGTGCCCCCCAGCCTGATCGT	Qy         421         GCACCCCCAGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	OY 481 TACCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA	Oy 541 GCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCCATGCGACAC	601	Qy 661 GAGTCGGACCTGCACCTGCGGAGATGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT	Qy 721 GTGCTCATCTTCAAGAAGCTGACAAGCTGTTCAGCGTACACAGATCGATGAGCTGGCC	Oy 781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 1	841	930	990	DD 1021 TCAGGTCTCAGCCAGGATGACCTGACAGCTGAGAGATCTCCCCAGGAGACGACTGAGATGCC  Qy 1021 TCAGGTCTCAGCCAGATGAGCTGACAGAGAGATCTCCCCAGGAGACGACTGCAGATGCC  DD 1110 TCAGGTCTCAGCCAGATGAGCTGACAGTGCAGAATCTCCCCAGGAGACGACTGCAGATGCC	OY 1081 ATGGCCGGAAGCTGAGGCCTTATGGAGGTACCCAGGAAGCCATGACTCATCC
	1217 CCACACCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGGGGACCAGGAACCCTG 1276 	1277 TGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCTGCCTTGGCTGACTGG 1336	1337 GTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTCCTTGCATCCCCAGC 1396	1397 TEGICITGATCCCTGCCAGGGCCCCTTCCTTCCTGCTCATGGTCTTCAGGTGGCCTGATCA 1456	1457 TGGAAAGTAAGGAGTTAACCTTCTGGAAGTGAACCCTGACTCCATCCCCTATT 1516 	1517 GCCACCCTAACCAATCATGCAAACTTCTCCCTCGGGGTAATTCAACAGTTAAAAGAA 1576 	1577 GCTTATCTTAAATGTATTGTATTGGGGGGGGGGCCCACTCTATGTTATGTTAAGG 1636 	1637 AGTIGGTICTGGTICTIGGCTGATGTICTGTATCTTAACATGACCACAGTTIGTAAGTAC 1696 	RESULT 3 AX747274 LOCUS AX747274 1785 bp mRNA linear PAT 20-JUN-2003	ITION Sequence SION AX747274 ON AX747274.	KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo. REFERENCE I Amari T. Carairama T. Otenki T. Wakamatan b. Cato H. Tekii C.	Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.	TITLE Full-length CDNA sequences JOURNAL Patent: BP 1308459-A 799 07-MAY-2003; Helix Research Institute (JP) ; Research Association for Biotechnology (JP)	FEATURES Location/Qualifiers  1.1785 /organism="Homo sapiens" /mol_type="mRNA"	94; DB 6; Length 1785;	vative         0;         Mismatches         2;         Indels         0;         Gaps         0;           CCTGGACACCCCGGCCATGGGACCTGGGACGTGGGACGTGGGACGTGGGACGTGGGACACCCCCGCCCAGCATCATGGCCTCCACGACATGGACATCAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGA

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Submitted (104-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) Whistophy and cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA full insert sequencing: Construction: Holix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- £ 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; Innotation: HRI and RAB.
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HETWYGSGLSQDELTVQISQETTADAIARKLRPYGAPGYPASHDSSFQGTDTDSSGAP
LLQVYC"
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Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matumura, K., Nakajima, Y., Mizumo, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satch, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakagawa, K., Okumura, K., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                              Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S., Yamanto, J., Isono, Y., Kawa-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanchori, K., Takahashi Fujii, A., Osohima, A., Kawakami, B., Suzuki, Y., Sugano, S., NBDO human cDNA sequencing project Isogai, T., Masuho, Y., Magai, K. and Isogai, T.
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/clone lib="KIDNE2"
/note="cloning vector: pME18SFL3"
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/db_xrefs"taxon:9606"
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/db_xref="GI:21750434"
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Isogai, T. and Yamamoto, J.
Direct Submission
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Makamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takashi,M., Kanda,K., Yokoi,T., Furuya,T., Kakka,E.,
Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,
Hiraoka,S., Chiba,Y., Ishida,M., Kananabe,M., Watanabe,M.,
Hiraoka,S., Chiba,Y., Ishida,M., Kanaha,M., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takabahi-Pujii,A.,
Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
Sasaki,N., Arita,M., Imose,N., Musabhino,K., Yuuki,H., Oshima,A.,
Sasaki,N., Arita,M., Imose,N., Momiyama,H., Ishida,M., Hakani,S.,
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Suluki,O., Nakagawa,S., Senoh,A., Mazoguchi,H.,
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Kumagai,A., Tanigami,A., Fujiwara,T., Yamada,K., Fujii,Y.,
Tashiro,H., Tanigami,A., Fujiwara,T., Yamada,K., Fujii,Y.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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121   GGCACCCGTAGACCAGACCCCTAGCCACCATGGGCCAGAGAGCATTACCTTC	661 GAGTCGGACCTGGACCTGCCGGAGATGGCTCCATGTCGAGCCGAGAAATTGAT 720  [

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http://www.chori.org/bacpac/home.htm
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Contact: vega@sanger.ac.uk
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Direct Submission
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AL356390

Human DNA sequence from clone RP11-344H11 on chromosome 1 Contains the NROB2 gene for nuclear receptor subfamily 0 (group B, member 2), the 5' end of a novel gene (FLJ12455), the NUDC gene fornuclear distribution gene C homolog (A. nidulans), a novel gene (FLJ34633), a ribosomal protein L12 (RPL12) pseudogene, a ribosomal protein L12 (RPL12) pseudogene, a ribosomal protein L32 (RPL32) pseudogene, a novel gene (FLJ34633), a nov CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromesome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group, Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a MAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (bases 1 to 140207)
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496. _726
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/gene="RR11-344H11.8"

join(21468. _22032,27482. .28803,29251. .29417)

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                                                                                                                                                                                                                                                                                                                                                                                                      AL356390.24 G1:21436506
HTG; DC2; FLJ12455; FLJ34633; NROB2; NUDC; RPL12; RPL32
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chrl
RP11-344H11 is from the library RPCI-11.2 of
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
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us-09-989-890-105.oligo.rge

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|dene="RPI1-344H11.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="Mprpghprpasgpprightedcletydkppgpppsrrtrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPDVKLKGIPVYPYPRATSPAPDADSCCKEPLADPPPMRHSLPSTFASSPRGSBEYYS
HEBSDLDCHEMGSGBNSSREIDVLIFRKLTELLEVONTOPPVFLEKTSKIS
DLISSITQDYHLDEDDDAEGRLWGIIR ISTRKSRARPQTSEGRSTRAAPPTAAPDSG
HETMVGSGLSQDELTVQISQETTADAIARKLRPYGAPGYPASHDSSFQGTDTDSSGAP
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10273. .110356,112510. .112713))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: ESTs: Em:BE798032.1
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codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82119 CGGCCAACAGGGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCACCCGTAGACCAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(82059. .83097,83683. .83757,84288. .84370)
gene="RP11-344H11.3"
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product="nuclear distribution gene C homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |locus_tag="RP11-344H11.3-001"
|standard_name="OTTHUMP00000004472"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAli3559.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1039; DB
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="novel protein"
                                                                                                                                                                                  74033. .84877
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Best Local Similarity 100.0%; Pr
Matches 1039; Conservative 0;
                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="NUDC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="NUDC"
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                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPSESGAERRDRAAQVGTAAATAVATAAPAGGGPDPEALSAFPGRHLSGLSWPQVVRSTLEEQGLHVHS
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AARRYACLVTLHRVVNESTVCLMMHERRQTLDLIAALALQALAEGGFAATAALAWRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKI TPLTLKEAYVQKLVKVCTDSDRWSLI SLSNKSGKNVELKFVDSVRRQFEFSIDSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="ribosomal protein L32 (RPL32) pseudogene" complement (join(53464. .53610,53925. .54274))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="RP11-344H11.8"
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Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
Compositions and methods relating to lung specific genes
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                         ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGCTGCGGACCC
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96626 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 96685
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                                                                                                                                                                                                                                                                                                                                                                                             95906 ATCTCTGCTCTGCTGAGCCGCCCTTGAGTCCCCCACCTGCTGCTGCTCTGGCGACCC
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                                                                                                                                                           95726 Arecececeredacacececececeacareredecerecacerredaaceredada
                                                                                                                                                                                                                            95786 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCCACCAAGCCGC
                                                                                                                                                                                                                                                                                                               95846 CGCACCCGTAGACCCCAAGGACCCCTGGCCACACAGGGCCAGAGAGATTACCTTC
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                                                                                                                                                                                                       CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC
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                                      DB 14;
                                    Score 937; DB
Pred. No. 0;
0; Mismatches
                                    54.7%;
                                                                             Conservative
                                                          Similarity
                                                                           Matches 1037;
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                                                                                                                                    Assembly program: XGRP4; version 4.58
Assembly program: XGRP4; version 4.58
Assembly program: XGRP4; version 4.58
Gequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q30
Consensus quality: 110681 bases at least Q20
Insert size: 111138; sum-of-contigs
Insert size: 11403; 8um-of-contigs
Coulity coverage: 11.23x in Q20 bases; sum-of-contigs Quality
Coverage: 10.67x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18958: contig of 18058 bp in length
1859 35144: contig of 16986 bp in length
1853 35244: gap of 100 bp
1854 35244: gap of 100 bp
1855 354710: contig of 19466 bp in length
1851 54810: gap of 100 bp
1851 72936: contig of 18126 bp in length
1852 95288: contig of 1885 bp in length
1853 95288: contig of 1985 bp in length
1859 95288: gap of 100 bp
1859 95288: gap of 100 bp
1859 108739: contig of 15751 bp in length
1869 111738: contig of 1855 bp in length
1860 111738: contig of 2899 bp in length
1860 111738: contig of 2899 bp in length.
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fragment chain:1"
35245. 54710
note="assembly fragment: 02786
fragment chain:1"
54811. 72936
/note="assembly fragment: 00223
fragment chain:2"
73037. 52888
/note="assembly fragment: 01820
fragment chain:2"
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fragment_chain:2
clone_end:8P6
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fragment_chain:2"
108840. _111738
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/note="assembly fragment:02048
fragment chain:1
clone_end:17
                                                        Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
/chromosome="1"
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                                                                                                                       Center project name: dJ426N7
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                     Center: Sanger Centre
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1263 ACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCCTG 1322
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot., D., Lamson, G., Dramac, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, I., Leshkowitis, D., Kita, D., Garcia, V. and Strache-Crain, B. Human genes and gene expression products
Patent: WO 0102568-A 177 11-JAN-2001;
CHIRON CORPORATION (9); HYSEQ, INC. (US)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                      Salceda,S., Macina,R.A., Recipon,H., Pluta,J., Sun,Y. and Liu,C. Compositions and methods relating to breast specific genes and proteins
                                                                                                                                                                                                                                                                                                                                                                  1203 GCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCTACAGAATGAAGAGGGG
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                                                                                                                                                                                                                                                                                        Query Match 22.1%; Score 378; DB 6; Length 386; Best Local Similarity 100.0%; Pred. No. 1.8e-207; Matches 378; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                           Patent: WO 02077232-A 104 03-OCT-2002;
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    .386
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/mol_type="unassigned DNA"
                                                                                                                                              Diadexus, Inc. (US)
Location/Qualifiers
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                             Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C. Compositions and methods relating to lung specific genes and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Euarchontoglires, Primates, Cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 385;
                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.5%; Score 385; DB 6; Le
100.0%; Pred. No. 1.5e-211;
ive 0; Mismatches 0;
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                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 02068633-A 55 06-SEP-2002;
Diadexus, Inc. (US)
Location/Qualifiers
                                                                                                                                            AX535028 385 bp 1
Sequence 55 from Patent WO02068633.
AX535028
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                    96746 TCAGGTCTCAGCCAGGATG 96764
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Homo sapiens
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Matches 385; Conservative
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RADOMIR CRYVENJAKOV, MARK DICKSON, SNEZANA DRMANAC, IVAN LABAT,
BADOMIR LESHKOWITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
BIRJIT STACHE CRAIN
C12N15/09, C12N15/09, C07K14/47, C07K14/82, C07K16/18, C12N1/15, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 300)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randaazo, F., Kennedy, G.C., Pot, D., Kannac, S., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., and Crain, B.S.
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140 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC C12N1/21,C12NS/10,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC Novel human genes and gene expression products ii FH Key Location/Qualifiers
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                                                               260 ATCTCTGGCTGTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGTGGGACCC
                                                                                                                                                                                                  241 TGGGTGTGGGAGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG
                                        121 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC
                                                                                                                      PR 28-JAN-1998 US 60/072910,24-PEB-1998 US 60/075954 | 31-MAR-1998 US 60/080515 PR 03-APR-1998 US 60/080515 PR 03-APR-1998 US 60/080666,21-OCT-1998 US 60/105234 PR PI LOUIS T WILLIAMS,JAIME ESCOBEDO,MICHAEL A INNIS,PABLO PI DOMINGEEZ GARCIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism='Homo sapiens (human)'
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                                                                                                                                                                                                                                                                                                                                                                                                                         BD212719 300 bp DNA linear Novel human genes and gene expression products ii. BD212719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human genes and gene expression products in Patent: JP 2002519000-A 861 02-JUL-2002; CHIRON CORP.HYSEQ INC CHIRON capiens (human) PN JP 2002519000-A/861 PP 02-JUL-2002 PP 28-JAN-1999 JP 200555580 PP 28-JAN-1998 US 60/072910,24-FEB-1998 US

    .300
    /organism="Homo sapiens"
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/db_xref="taxon:9606"

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JP 2002519000-A/861.
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Homo sapiens
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BD212719
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                                                                                                                                                                                 864
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                                                                                                                                                                                                                                                                                                                                                                                     200
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                                                                                                                                                                                                                                                                                                                                             AGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACGCCT 984
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, I., Leshkowitiz, D., Klta, D., Garcia, V. and Strache-Crain, B. Human genes and gene expression products
Patent: WO 0102568-A 2132 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                          CTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCG
                                                                                                                                                                                 805 CTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTG
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                                                                                               19.5%; Score 334; DB 6; Length 393; 100.0%; Pred. No. 7.3e-182; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.7e-174;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
/mol type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX071660 427 bp DN Sequence 2132 from Patent WO0102568.
                     1. .393
/note="n = A,T,C or G"
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db_xref="taxon:9606"
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                                                                                                                      Best Local Similarity 100.
Matches 334; Conservative
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/db_xref="taxon:9606"
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Location/Qualifiers
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JP 2002519000-A/4887
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                                                                         Best Local Similarity 99.7
Matches 299; Conservative
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Human gene and gene expression product I

Patent: JP 200250010-A 34 08-JAN-2002;

CHIRON CORP, HYSEQ INC
OS Home sapiens (human)

PN JP 200250010-A/34

PD 08-JAN-2002

PF 22-DEC-1998 US 60/106875, 03-APR-1998 US 60/105877 PR
21-DEC-1998 US 60/105234, 27-OCT-1998 US 60/105877 PR
21-DCT-1998 US 60/105234, 27-OCT-1998 US 60/10587 PR
21-DCT-1998 US 60/105234, 27-OCT-1998 US 60/10587 PR
21-DCT-1998 US 60/105234, 27-OCT-1998 US 60/10587 PR
21-DCT-1998 US 60/105234, 27-OCT-1998 US 60/10587 PR
21-DCT-1998 US 60/105234, 27-OCT-1998 US 60/10587 PR
21-DCT-1998 US 60/10524, 27-OCT-1998 US 60/10587 PC
212N15/09, C12N15/09, C07X14/47, C07X14/705, C12N1/15, C12N1/19, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Honindae; Homo.

10 (bases 1 to 300)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C. Giese, K., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., and Crain, B.S.
                                                                                                                                                                                                                                                                                                                         C12N15/09, C12N15/09, C07K14/47, C07K14/705, C12N1/15, C12N1/19, PC
                                                                                                                                                                                 CTCGGAGGGTCGTTCAACTCGGGCTGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCA 1004
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                                                                                                                                                                                                                                                     1005 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGA 1064
                                                                                                                                                                                                                                                                                         240
                                                                                                                            CGGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCCACAGAC 120
                                                                                                                                                                                                  CTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCA 180
                                   884
                                                                                                         944
                                                                     9
                                                      CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGG
                                                                                                         CCGCCTGGTACGCGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGAC
                                                                                                                                                                                                                                                                              181 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCCAGGA
                                     CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGGATGCTGAGGG
 Gaps
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Location/Qualifiers
 Indels
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Key
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Human gene and gene expression product I.
BD128735
 Mismatches
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,C12Q1/68,C12N15/00,
PC C12N5/00,C12N15/00
CC Human gene and gene
FH Key Local
FT Source 1.
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JP 2002500010-A/34.
Homo sapiens (human)
Homo sapiens
 Conservative
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300;
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 Matches
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VERSION
KEYWORDS
SOURCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                       BD128735
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                                                                                                                                                                                                                                                                                                                                        180
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                                                                                               740 TGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCCAAGTGCACATCAGACACTG 799
                                                                                                                                                                                              859
                                                                                                                                                                                                                          61 TGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACC 120
                                                                                                                                                                                                                                                                                           919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCTGCTGCCCCTGACAGTGGCCCATGAGACCATGGTGGGTCAGGTCTCAGCCAGGATG 300
                                                                                                                                            9
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                   181 GAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCAA
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                                                                                                                                                                                            TGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACC
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                                                  Gaps
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  Length 300;
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                                               Indels
14.5%; Score 249; DB 6; I
99.7%; Pred. No. 2.2e-132;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 116 from Patent WO02068633. AX555089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaretne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="MGI:1916323"
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PWPSLLPHGTACLAPSPTAPAALRSTTPSMNRTWTCLRWAVAPCRAGRSTCLFSRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="MGC:11921 IMAGE:3599314"
/tissue type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone lib="NCI CGAP_Mam6"
/lab_host="DH108"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: p Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19526881.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (27-AR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing Destrict College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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RADOMIR CRKVENJAKOV, MARK DICKSON, SNEZANA DRMANAC, IVAN LABAT,
DENA LESHKOWITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
BIRJIT STACHE CRAIN
C12N15/09, C12N15/09, C07K14/47, C07K14/82, C07K16/18, C12N1/15,
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1 (bases 1 to 1680)

Straubberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buctow, K. H., Schaffer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Mang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ברטטפשטט 1680 bp mRNA linear ROD 29-JUN-2004
Mus musculus RIKEN cDNA 1810019J16 gene, mRNA (cDNA clone MGC:11921
IMAGE:3599314), complete cds.
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                                                                                                                          Hominidae, Homo.

I (bases 1 to 7208)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V., Jones, L.W. and Crain, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMINGUEZ GARCIA,
PI JULIE SUDDUTH KLINGER, CHRISTOPH REINHARD, KLAUSE GIESE, FILIPPO
                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS 60/075954 PR
60/080515 PR
60/105234 PR
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                                                                                                                                                                                                                                                                                                                                                                                                                            OS Homo sapiens (human)
PN JP 2002519000-A/4887
PD 02-JUL-2002
PF 28-JAN-1999 US 60/072910,24-FEB-1998 US 60/095954
31-MAR-1998 US 60/080114,03-APR-1998 US 60/080515 PR 60/-24-1998 US 60/080666,21-0CT-1998 US 60/080666,21-0CT-1998 US 60/105234 PR 28-0CT-1998 US 60/105877
PI LOUIS T WILLIAMS, JAIME ESCOBEDO, MICHAEL A INNIS, PABLO
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100.0%; Pred. No. 1.6e-09;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       Novel human genes and gene expression products ii
Patent: JP 2002519000-A 4887 02-JUL-2002;
PHIRON CORP, HYSEQ INC
OS Homo sapiens (human)
PN JP 2002519000-A/4887
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/db_xref="taxon:9606"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMEL, SM.; SMYSENGY, Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as attempt was made to resolve all sequencing problems, such as attempt was made to resolve all sequencing problems, such as attempt was made to resolve all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly we confirmed by restriction digest, except on the rare occasion of
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RP23-137L22 is from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.

Por further details see http://www.chori.org/bacpac/home.htm

VBCTOR: pBACe3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
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                                                                                                                                                                                                                                                                                                             AL627228 193813 bp DNA linear ROD 04-FEB-2003
Mouse DNA sequence from clone RP23-137L22 on chromosome 4, complete
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Submitted (04-FEB-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requeste: clonerequest@sanger.ac.uk
On Feb 4, 2003 this sequence version replaced gi:22474404.
                                                             Gaps
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  Length 1680;
                                                             0; Indels
                                                                                                                                            885 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 922
                                                                                                                     835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
  Query Match
2.2%; Score 38; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 38; Conservative 0; Mismatches 0;
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Contact: humquery@Banger.ac.uk
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/db_xref="taxon:10090"
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Location/Qualifiers
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/clone_lib="RPCI-23"
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
                                                                                                                                                                                                                                                                           BC079148 1718 bp mRNA linear ROD 15-SEP-2004 Rattus norvegicus similar to hypothetical protein FLJ34633, mRNA (cDNA clone MGC:94165 IMAGE:7128510), complete cds.
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Submitted (102-MOGC), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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104723 Arcaccaccarcaccaccaccaccaccaccaccaccacca 104760
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
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2.2%; Score 38; DB 9; Length 193813;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Murinae; Rattus.

2. (bases 1 to 215419)

3. Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Anglando, D., Allen, C., Allen, H., Albbrooks, S., Amin, A., Angulano, D., Anglebechi, V., Aoyagi, A., Barber, M., Baca, B., Baden, H., Balardaniake, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Balawin, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, G., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Derger, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Harnandez, S., Finley, M., Hamil, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Lio, C., Lio, C., Lio, C., Lio, C., Lio, C., Lio, 
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Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
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YPDVKLKGIPVYPYRHATSPVPDADSCCKEPLADPPPTRHSLPSTFTSSPRGSEEYYS
FHESDLDLPEMGSGSMSSREIDVLIFKKLTELFSVHQIDELAKCTSDTVFLEKTSKIS
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LQVYC"
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PDPKDPGHHGPESITFISGSAEPANEPPTCCLLWRPWGWDWCRAAFCPRRCRDCLQRC
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product="similar to hypothetical protein FLJ34633"
/protein id="AAH79148.1"
/db_xref="G1:50927713"
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100.0%; Pred. No. 0.00028;
ive 0; Mismatches 0; Indels
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                                                                                     'note="Vector: pExpress1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GeneID:313018"
                                                                                                                                                                                                                                                                                                             db_xref="GeneID:313018"
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                                                                                                                                                                                                                                                                                gene="MGC94165"
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Best Local Similarity 100.
Matches 29; Conservative
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Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Nov 9, 2002 this sequence version replaced gi:22772470.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.lcm.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Litu, J., Litu, W., Litu, Y., London, P., Longacre, S., Lopez, J.,

Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,

Mahcshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,

Manhiney, S., McLeod, M.P., Moneil, T.Z., Menemen, E.,

Manhiney, S., McLeod, M.P., Moneil, T.Z., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Munidemas, M., Murphy, M., Nair, L.,

Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,

Pagternak, S., Paul, H., Perez, A., Perez, L., Fennocch, C.,

Plopper, F., Poindexter, A., Perez, L., Fennocch, C.,

Ryally, B., Railly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rilly, B., Railly, M., Ren, Y., Reuter, M., Richards, S., Shen, H.,

Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,

Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,

Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,

Sheimle, M., Strong, R., Sutton, M., Svatek, A., Trejos, Z., Usmani, K.,

Valas, R., Vera, V., Villaana, D., Walker, R., Wang, Y.,

Wang, Q., Wanre, S., Warren, R., Wei, X., White, F.,

Williams, G., Wallson, R., Wu, J., Yakub, S., Yen, J., Yoon, V.,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Smith, D., Von, N.,

Wiener, Shhiesis, R., Smith, D.R., Buth, R., Smith, H.O.,

Nicelerhausern, A., Weiss, R.,

Shhire, Shhiesis, R.,
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 235419)
Worley, K.C.
Worley, K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project Information
Center project name: GBBU
Center clone name: GR20-11020
Center clone name: CH220-11020
Center clone name: CH230-11020
Assembly program: Phrap; version 0.990329
Consensus quality: 225536 bases at least Q40
Consensus quality: 228649 bases at least Q20
Consensus quality: 228649 bases at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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COMMENT

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Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 24946)

Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Alalen, C., Allen, H., Alabrooks, S., Amin, A., Agaman, D., Bach, H., Barnstead, M., Benamed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benamed, F., Biwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bulay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cleveland, C., Cockrell, R., Cox, Coyle, M., Cree, A., D'Souwa, L., Davis, C., Coyle, M., Cree, A., D'Souwa, L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Eyen, M., Cree, A., Dinh, H., Divya, K., Egan, A., Escotto, M., Eugene, C., Evans, C., Frans, C., Frane, C., Evans, C., Frane, C., Frane, C., Frane, C., Evans, C., Frane, C., Evans, C., Frane, C., Frane, C., Frane, C., Frane, C., Frane, C., Frane, C., Frane, C., Frane, Fraser, C.M., Gabisi, A., Ganda, R., Garda, A., Garder, M., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Havlak, P., Havlak, P., Havlak, P., Havlak, P., Havlak, P., Havlak, P., Henderson, N., Hernandez, J.,
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Ratius norvegicus clone CH230-180E4, WORKING DRAFT SEQUENCE.
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                               1 221492: contig of 221492 bp in length 3 221592: gap of unknown length 3 228631: contig of 7059 bp in length 2 228751: gap of unknown length 2 238751: contig of 6668 bp in length 1 Costion/Qualifiers
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AC118963.4 GI:25009106
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
RATUH NOTVEGICUS (NOTWAY rat)
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site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end_sequence:BH344795"
219911. .220573
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Submitteel (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23269749.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgs..bm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Holling, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacoco, L., Janag, H., Obnson, B., Johnson, R., Johlson, R., Johlson, R., Johlson, R., Johlson, B., Johnson, R., Johlson, R., Johlson, C., Karpathy, S., Kelly, S., Khan, Z., King, L., Li, Z., Liu, J., Liu, W., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Liu, X., Ma, J., Lousesgel, H., Lozado, R.J., Lu, X., Ma, J., Mangum, P., Martin, K., Martin, R., Martinez, E., Milosavi, E., Mangum, P., Martin, K., Martin, R., Martinez, E., Milosavi, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavi, S., McLeod, M.P., McNeill, T.Z., Mencen, E., Moore, S., Milosavi, E., Noal, D., Newton, N., Nguyen, N., Norris, S., Nankelmeh, O., Okwonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasteris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Paul, H., Perez, A., Popovic, D., Primus, E., Pul, L.-L., Plazo, M., Oulroz, J., Rachlin, E., Reeves, K., Regier, M., Reilly, R., Reilly, M., Ren, Y., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutcer, S., Tingey, A., Tabor, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Tabor, P., Taylor, T., Yonn, W., Walas, R., Warzen, J., Walzen, R., Weillson, R., Walzen, R., Walzen, W., Walzen, R., Walzen, W., Walzen, R., Walzen, S., Wanzen, J., Wanzen, R., Walze, R., Wanzen, J., Yon, W., Walze, R., Wanzen, J., Yaho, S., Dunn, D., von, N., Yu, F., Shang, J., Zhang,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Assembly program: Phrap; version 0.990329
Consensus quality: 213357 bases at least Q40
Consensus quality: 215358 bases at least Q30
Consensus quality: 215358 bases at least Q30
Estimated insert size: 223109; aum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.
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253568
253668
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TITLE
JOURNAL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai, Bucheria; Buarchoncoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Muridae; Rattus.

Sciurognathi; Muroidae; Muridae; Murinae; Rattus.

I (bases I to 256017)

Sciurognathi; Muroidae; Muridae; Murinae; Rattus.

I (bases I to 256017)

Muzny, D.M., Adama, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Arc, J.R., Ayele, M., Banks, T., Burch, P., Burkett, C., Burkenburg, K., Bonnin, D., Buhay, C., Burch, P., Burkett, C., Murrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavaz, D., Chavaz, D., Chan, Z., Chon, Z., Chock, M.D., Dathorne, S.R., David, R., Davis, C., Coy, C., Coy, Carroll, L., Dederich, D.A., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Davis, C., Davy-Carroll, L., Dederich, D.A., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Bannatt, C., Edgar, D., Elagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garis, A., Garner, T., Garza, N., Gall, R., Garner, T., Garza, N., Gall, R., Garner, T., Garza, N., Garli, R., Hernandez, O., Hodeson, A., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hodeson, A., Hart, M., Havlak, P., Hawes, A., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Luzier, M., Massey, E., Martin, R., Martina, R., Martina, R., Massey, E., Marken, M., Masue, P., Martin, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., Martina, R., M
                     NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC126312 256017 bp DNA linear HTG 13-NOV-2002
Rattus norvegicus clone CH230-1B9, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 0.00031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .249406
/organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-180E4"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/note="wgs_contig"
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Matches 29; Conserva
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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g 6

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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:23267435.

The sequence in this assembly is a combination of BAC based reads and whole genome shocyun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, R., Tamerisa, A., Tamerisa, R., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, D., Villalon, D., Vinson, R., Wang, Q., Williams, G., Williams, M., Ward, W., W., Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Roscyk, R., Meinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley,K.C.
Direct Submission
Submitted (05-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256017)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Phrap; version 0.990329
Consensus quality: 214827 bases at least Q40
Consensus quality: 219116 bases at least Q30
Consensus quality: 221911 bases at least Q20
Estimated insert size: 222841; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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22 83821: gap of unknown length
22 253567: contig of 169746 bp in length
58 253667: gap of unknown length
68 255617: contig of 2350 bp in length.
Location/Qualifiers
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-1B9
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Unpublished
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PAT 06-AUG-2001
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                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee,J., Thompsho,P. and Lillie,J. Identification, and therapy of ovarian
                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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                                                                                                                                            Schlegel, R., Deeds, J., Berger, A. and Zhao, X. Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer assessment, prevention, and therapy of cervical cancer Patent: WO 014457-A 712 14-JUN-2001; Millennium Predictive Medicine, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 26; DB 6; Length 91;
100.0%; Pred. No. 0.015;
cive 0; Mismatches 0; Indels
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Millennium Predictive Medicine, Inc.
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                                                                                                                                                                                                                                                           1. .329
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1686 TTTGTAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 from Patent WO0118542. AX098107
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     AX185017.1 GI:15136393
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                                       Homo sapiens (human)
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Best Local Similarity 100.0
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
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AX098107/c
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therappy of cervical cancer
Patent: WO 0142467-A 1200 14-JUN-2001,
Millennium Predictive Medicine, Inc. (US)
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100.0%; Pred. No. 0.001;
trive 0; Mismatches 0; Indels
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-1B9"
6668. .7475
/note="clone_boundary
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    .323
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                           /estimated length=unknown 83822. .85574
/note="wgs_contig"
219978. .221353
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38358. 39527
/note="wgs_contig"
67950. 69005
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253568. .253667
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78781. .81213
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3722. .83821
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Best Local Similarity 100.0%
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AX185017/c
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Best Local Similarity
Matches 25; Conserv
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CQ505617/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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'Aammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                         Schlegel, R., Deeds, J., Berger, A. and Zhao, X. Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 1358 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 014267-A 2181 14-JUN-2001,
Millennium Predictive Medicine, Inc. (US)
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100.0%; Pred. No. 0.015;
ive 0; Mismatches 0; Indels
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AX186486
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                                                                                                                                         1. .203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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CQ424843.1 GI:41377072
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Best Local Similarity 100.
Matches 26; Conservative
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Genes differentially expressed in human prostate cancer and their
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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denes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer patent: WO 0170979-A 17410 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 9877 19-JUL-2001, Millennium Pharmaceuticals, Inc. (US)
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Pred. No. 0.015;
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llarity 100.0%; Pred. No. 0.057;
Conservative 0; Mismatches 0; Indels
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37484 from Patent WO0160860.
CQ505617
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Sequence 17410 from Patent WO0170979.
CQ410339
                                                                                                                                                                                                                                           Query Match 1.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
                                                                                              1. .576
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/db_xref="taxon:9606"

    255
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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                                                                          Location/Qualifiers
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PAT 23-JAN-2004
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 6873 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                         Lee,J. and Lillie,J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer batent: WO 0170979-A 11387 27-5EP-2001;
Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.057;
tive 0; Mismatches 0; Indels
    Length 310;
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Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels
1.5%; Score 25; DB 6; Le
ilarity 100.0%; Pred. No. 0.057;
Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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                                                                                                  280 GTAAGTACCTCGGCCGCGACCACGC 304
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                      Similarity
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CQ421839/c
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 5095 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers
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                                                                                            1.5%; Score 25; DB 6; Length 275;
100.0%; Pred. No. 0.057;
tive 0; Mismatches 0; Indels
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Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                              DNA
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Sequence 5095 from Patent WO0170979.
CQ398024
                                                                                                                                                                                                                                                                                                          304 bp Di
Sequence 7524 from Patent WO0160860.
/organism="Homo sapiens"
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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CQ475657.1 GI:41441276
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Best Local Similarity 100.03
Matches 25; Conservative
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                                                                                                                  Best Local Similarity
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VERSION
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CQ475657/c
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CQ398024
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PAT 20-APR-2005

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AUTHORS TITLE

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REFERENCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                   Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
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Immune-related proteins and the regulation of the Patent: WO 031002599-A 15 09-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
                     linear
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Berka,R., Bashkirova,E. and Rey,M.
Methods for monitoring multiple gene expression
Patent: WO 2005030998-A 1051 07-APR-2005;
Novozymes Biotech, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 0.22;
tive 0; Mismatches
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          Sequence 1051 from Patent WO2005030998.
CS067068
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Sequence 17222 from Patent WO0170979.
CQ410151 GI:41317932
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                                                                                                                                                                                                                                                                                                                                          /organism="Hypocrea jecorina"
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Homo sapiens
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Best Local Similarity 100.0
Matches 24; Conservative
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 995 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 0.058;
tive 0; Mismatches 0; Indels
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Sequence 985 from Patent WO0142467.
AX185290

    .463
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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DEFINITION ACCESSION

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                          Lee,J. and Lillie,J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 17222 27-EEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification,
Genes, compositions, and therapy of ovarian cancer
Patent: WO 01709-A 534s 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Sequence 11632 from Patent WO0170979.
CQ404561
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Sequence 5345 from Patent WO0170979.
CQ398274
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/organism="Homo sapiens"
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CQ398274/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 11632 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 100.0
Matches 24; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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100.0%; Pred. No. 0.22;
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100.0%; Pred. No. 0.22;
vative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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                                                                                          1690 TAAGTACCTCGGCCGCGACCACGC 1713
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Best Local Similarity 100.
Matches 24; Conservative
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CQ395905/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 9991 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer batent: WO 0170979-A 4074 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 9991 from Patent WO0170979.
CQ402920
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    .310
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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CQ397003/c
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 5545 19-UUL-2001,
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
assessment, prevention, and therapy of cervical cancer
Patent: WO 014467-A 9 14 JUN 2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Sequence 5545 from Patent WO0151628.
CQ420511
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                                    AX185234 331 bp 1 Sequence 929 from Patent WO0142467.

    .331
    /organism="Homo sapiens"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Matches 24; Conservative
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AX185287/c
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer patent: WO 0170979-A 9305 27-SEP-2001,
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Larity 100.0%; Pred. No. 0.22;
Conservative 0; Mismatches 0; Indels
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                                                                                                                       Sequence 9305 from Patent WO0170979. CQ402234
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1690 TAAGTACCTCGGCCGCGACCACGC 1713
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CQ410876/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                   Lee, J. and Lillie, J.

Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 4711 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
| J. 368 | /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"
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100.0%; Pred. No. 0.22;
tive 0; Mismatches
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Sequence 5958 from Patent WO0170979.
CQ398887
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CQ403939/c
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                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes differentially expressed in human prostate cancer and their
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100.0%; Pred. No. 0.22;
ive 0; Mismatches 0; Indels
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Sequence 4711 from Patent WO0170979.
CQ397640

    .346
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                             Gaps
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 12238 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 5958 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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                                                                                                                                                            DB 6; Length 370;
0.22;
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       Sequence 12238 from Patent WO0170979.
                                                                                                                                                            Query Match
1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 24; Conservative 0; Mismatches

    .370
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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AUTHORS
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therappy of ovarian cancer
Patent: WO 0170979-A 16765 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 2902 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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1.4%; Score 24; DB 6; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels
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Sequence 2902 from Patent WO0170979.
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/organism="Homo sapiens"
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/db xref="taxon:9606"
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/mol_type="unassigned DNA"
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CQ395831.1 GI:41303612
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CQ409694.1 GI:41317475
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PAT 23-JAN-2004
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 3267 27-SEP-2001, Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 0.22;
tive 0; Mismatches
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Pred. No. 0.22;
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Sequence 3267 from Patent WO0170979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity
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ACCESSION
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ACCESSION
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CQ396196/c
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CQ402521/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 9231 27-5EP-2001; Millennium Pharmaceuticals, Inc. (US)
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           DB 6; Length 391;
0.22;
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100.0%; Pred. No. 0.22;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                              linear
                                               0; Indels
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Sequence 16375 from Patent WO0170979.
CQ409304
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Sequence 9231 from Patent WO0170979.
1.4%; scc. 100.0%; Pred. No. c. 0; Mismatches
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                                                                               1690 TAAGTACCTCGGCGGCGACCACGC 1713
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                                                                                                      30 TAAGTACCTCGGCCGCGACCACGC 7
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                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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     Query Match
Best Local Similarity 100.(
Matches 24; Conservative
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Best Local Similarity 100.0
....nea 24; Conservative
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ORGANISM
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CQ409304/c
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TITLE
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RESULT 66

1690 TAAGTACCTCGGCCGCGACCACGC 1713

CQ476176/c

DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

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PAT 23-JAN-2004
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                     Lee,J. and Lillie,J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therappy of ovarian cancer betent: WO 0170979-A 17159 27-SEP-2001, Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Genes, compositions, kits, and method for identification,
Genes, compositions, hits, and therapy of ovarian cancer
Patent: WO 0170979-A 521 27-58P-2001,
Millennium Pharmaceuticals, Inc. (US)
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
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100.0%; Pred. No. 0.22;
iive 0; Mismatches
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CQ404437
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                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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CQ398150.1 GI:41305931
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                       sapiens (human)
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                                          Homo sapiens
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Best Local Similarity
Matches 24; Conserv
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CQ398150/c
LOCUS
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LOCUS
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes differentially expressed in human prostate cancer and their
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                       linear
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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CQ410088.1 GI:41317869
            404 bp Di
Sequence 8043 from Patent WO0160860.
CQ476176
CQ476176.1 GI:41441795
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CQ408978
                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="unassigned DNA"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                   1. .404
/organism="Homo sapiens"
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Homo sapiens
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CQ408978/c
LOCUS
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ACCESSION VERSION KEYWORDS SOURCE

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AUTHORS TITLE

REFERENCE

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FEATURES

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CQ410088/c

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Length 420;

PAT 23-JAN-2004

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Schlegel, R., Endege, W.O. and Monahan, J.E. Genes differentially expressed in human prostate cancer and their
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 1710979-A 5813 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
Patent: WO 0170979-A 15689 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                     1.4%; Score 24; DB 6;
100.0%; Pred. No. 0.22;
ative 0; Mismatches
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100.0%; Pred. No. 0.22;
tive 0; Mismatches
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Sequence 5813 from Patent WO0170979.

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/db_xref="taxon:9606"
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                                        Location/Qualifiers
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CQ507382.1 GI:41473592
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CQ507382/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                               Lee, J. and Lillie, J. Genes, and method for identification, Genes, compositions, kits, and herappy of ovarian cancer sasessment, prevention, and therappy of ovarian cancer Patent: WO 0170979-A 11508 27-SEP-2001, Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 15689 from Patent WO0170979.
CQ408618.1 GI:41316399
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                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes differentially expressed in human prostate cancer and their
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Sequence 18622 from Patent WO0170979.
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CQ506077
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    Pred. No. 0.22;
Best Local Similarity 100.0%; Pred. No. 0.2 Matches 24; Conservative 0; Mismatches
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CQ411551.1 GI:41319332
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Genes differentially expressed in human prostate cancer and their
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 18496 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                                                                   DB 6; Length 424;
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   426 bp DNA Sequence 18496 from Patent WO0170979. CQ411425
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/mol_type="unassigned DNA"
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PAT 23-JAN-2004
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                  Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 18016 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.22;
tive 0; Mismatches
442 bp DNA
Sequence 18016 from Patent WO0170979.
CQ410945
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Sequence 15845 from Patent WO0170979.
CQ408774
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    442
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                            CQ410945.1 GI:41318726
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                                                                                                                                                                                                                  Lee, J. and Lillie, J.
                                                                                                Homo sapiens (human)
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CQ397235/c
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Location/Qualifiers
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100.0%; Pred. No. 0.22;
iive 0; Mismatches 0; Indels
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                                                                                            437 bp DN Sequence 3100 from Patent WO0170979. CQ396029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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      56 TAAGTACCTCGGCGCGACCACGC 33
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CQ402355.1 GI:41310136
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24; Conservative
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Best Local Similarity
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CQ410945/c
                                                                                CQ396029/c
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PAT 30-JAN-2004
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                   Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                    Length 446;
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                                                                            Patent: WO 0160B60-A 36059 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Millennium Predictive Medicine, Inc. (US)
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100.0%; Pred. No. 0.22;
ive 0; Mismatches
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CQ506124
CQ506124.1 GI:41472250
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    .446
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                           Lee,J. and Lillie,J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 4306 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 10610 27-EEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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0.22;
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CQ504192
CQ504192.1 GI:41470221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQ403539 446 bp DNA Sequence 10610 from Patent WO0170979.
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                                                                                                                                                                                                                                                                                   /mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .446
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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CQ403539.1 GI:41311320
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 24; Conservative
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Matches 24; Conserva
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SOURCE

CQ403539/c DEFINITION ACCESSION VERSION KEYWORDS

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Query Match

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AUTHORS TITLE JOURNAL

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CQ504192/c LOCUS

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PAT 24-OCT-2002
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therappy of ovarian cancer
Patent: WO 10979-A 18705 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches (
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Sequence 18705 from Patent WO0170979.
CQ411634
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LOCUS CQ396273 464 bp DN
DEFINITION Sequence 3344 from Patent W00170979.
                                                                                                       AX523478 457 bp D
Sequence 66 from Patent WO02064788.
AX52478
AX523478.1 GI:24412374
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/db_xref="taxon:9606"
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Best Local Similarity 1
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AUTHORS
                                            RESULT 89
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VERSION
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|protein id="CACO4516.1"
|db_xref="G1:909727"
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|db_xref="UniProt/TrENBL:Q9F433"
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Submitted (22-AUG-2000) Yang S., Life Science, National Tsing Hua
University, 101, Section 2 Kuang Fu Road, Heinchu, 300, TAIWAN
Location/Qualifiers
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EVGA gene; positive transcription regulator EVGA.
Klebsiella pneumoniae
Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Identification of genes present specifically in a virulent strain of Klebsiella pneumoniae
Infect. Immun. 68 (12), 7149-7151 (2000)
                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Pred. No. 0.22;
ive 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/strain="CG43"
Millennium Predictive Medicine, Inc. (US)
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/country="Taiwan"
/note="isolated from blood
contig region pSL042"
complement (26. .322)

    .446
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/gene="EVGA"
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/codon_start=1
/trans1_table=11
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                                    Location/Qualifiers
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2 (bases 1 to 450)
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PAT 23-JAN-2004

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                             Lee, J. and Lillie, J. Genes, compositions, kits, and method for identification, Genes, compositions, kits, and therapy of ovarian cancer Patent: WO 0170979-A 15851 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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Patent: WO 0170979-A 4472 27-SEP-2001,
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                      Length 471;
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100.0%; Pred. No. 0.22;
tive 0; Mismatches
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
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Sequence 10775 from Patent WO0170979.
CQ403704
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Sequence 4472 from Patent WO0170979.

    .471
    /organism="Homo sapiens"
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/organism="Homo sapiens"
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                                           Hominidae; Homo.
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                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 3344 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 9665 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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1.4%; Score 24; DB 6; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.22;
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CQ408780
CQ408780.1 GI:41316561
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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CQ396273
CQ396273.1 GI:41304054
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Homo sapiens
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Best Local Similarity
                                                                                    Homo sapiens
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SOURCE

AUTHORS REFERENCE

TITLE

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DEFINITION

ACCESSION VERSION KEYWORDS

CQ402594/c

RESULT 92

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RESULT 93 CQ408780/c LOCUS

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Matches

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PAT 23-JAN-2004

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 15976 27-SEP-2001,
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification,
Genes, revention, and therapy of ovarian cancer
Patent: W0.179979-A 4993 27-5EP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Sequence 4993 from Patent WO0170979.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 836 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
compositions, kits, and method for identification,
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              assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 10775 27-SEP-2001, Millennium Pharmaceuticals, Inc. (US)
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Sequence 16367 from Patent WO0170979.
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Sequence 836 from Patent WO0142467.
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 017099-A 11286 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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1.4%; Score 24; DB 6; Length 521;
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Matches 24; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels
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The invention relates to a novel isolated nucleic acid molecule comprising: a sequence encoding a sequence comprising 11-1518 amino acids ; a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides of the invention can be used to treat disorders by gene therapy. This polynucleotide represents a breast specific related sequence of the invention
                                                                              New isolated nucleic acid molecule, useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer
Liu C;
Sun Y,
Pluta J,
                                                                                                                                                             Claim 1; Page 250-251; 377pp; English.
Recipon H,
Macina RA,
                                    WPI; 2003-018927/01.
                                                                                                                         in a patient.
Salceda S,
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1713; 0; Gaps	GGACCGTGGC            GGACCGTGGC	CCACCAAGC	AGCATTACC:	SCTCTGGCGAC	GATTGCCTCC 	SGACTCCACTC	DAGCCCTGATC	DAGCAGCTTC             	GCCACCTCCC	ACCCATGCGA(               ACCCATGCGA(	CTATTCTTTCC 	CCGAGAAATTC
8; Length 0; Indels	CTCCACGCTT            CTCCACGCTT	CACCTCAGCC	PATGGGCCAGA(               PATGGGCCAGA(	CCTGCTGCCT             CCTGCTGCCT		TGTCTACTGA            TGTCTACTGA	KAAGTGCCCCC                KAAGTGCCCCC	CAACCATGGG	CCTACCCGAG             CCTACCCGAG	CCGATCCCCC	CCGAGGAGTA(              CCGAGGAGTA(	CCATGTCGAG
Score 1713; DB Pred. No. 0; 0; Mismatches	ATGCCCCGCCCTGGACACCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAGG	CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCGC 	CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC	ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGCTTGGCGACCC	TGGGTGTGGGAGTGCCGGGGTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG	CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG 	GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 	GCACCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCAGCTTTAGC 	TACCCCGATGTTAAGGTCAAGGATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 	GCCCTGATGCGGACTCCTGCTGCAAGGACCACTGGCGATCCCCCACCCA	AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT	GAGTCGGACCTGGACGAGATGGGCAGTGGCTCCATGTCGAGCCGAAATTGAT
0%; Score 0%; Pred. 0; Mist	ACCCCCCCCC                   ACCCCCGCCCC	GTCTGGAGACA           GTCTGGAGACA	accccaagga(            accccaagga(	AGCCGGCCCT.            AGCCGGCCCT.	GCCGGGCTGC           GCCGGGCTGC	TGCGGGGATG(            TGCGGGGATG(	ACTGGGCCAA(            ACTGGGCCAA(	GGGATGGCCA(             GGGATGGCCA(	TCAAAGGCATO	CCTGCTGCAA(            CCTGCTGCAA(	TTGCCAGTAG:            TTGCCAGTAG	TGCCGGAGAT
uery Match 100.0%; est Local Similarity 100.0%; atches 1713; Conservative (	CGCCCTGGAC                  CGCCCTGGAC	ACAGAGCTAT            ACAGAGCTAT	CGTAGACCAG             CGTAGACCAG	GCTCTGCTG            GGCTCTGCTG	TGGGAGTGGT            TGGGAGTGGT	GGAGCCTGTG             GGAGCCTGTG	GCTGAAGCCA             GCTGAAGCCA	cccagccggc             cccagccggc	GATGTTAAGC              GATGTTAAGC	GATGCGGACT              GATGCGGACT	CCCAGCACCT              CCCAGCACCT	GACCTGGACC
similar 13; Con												
uery Match est Local atches 171	п п	61	121	181	241	301	361	421	481	541	601	661

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ò	721	GTGCTCATCTTCAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC 78	80
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È	781	81	40
අු	781	AAGTGCACATCAGACACTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 84	0
8 1	841	AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGATGAGGGCCGCCTGGTACGCGGC 90	8 8
a (	841	AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGGCCGCCTGGTACGCGGCC 9C	- :
රි ස්	901	ATCATTICGCATTAGTACCCGAAAGAGCCGTGCTCGCCCAAGACCTCGGGGGGGTCGTTCA 96 ALCATTICGCATTAGTACCCGAAAGAGCCGTGCTCGCCCCAAGACCTCGGGGGGGG	9 9
8 8	106	AICALICGCALIAGIACCCGAAAAGAGCCGGCCCCCCCCCC	2 6
<u>e</u>	961	961 ACTOGGGCTGCTGCCCCAACCGCTGCTGCCCTGAAACATGAGACATGAGGGCC 102.	1020
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qq	1021	TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCC 10	080
ò	1081	ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATT	140
qq	1081	ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 11	140
È	1141	TTCCAGGGCACCGACACAGACTCGTCGGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC 12	200
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Ġ	1261		320
op Q	1261	GGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCC 13	320
ò	1321	TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 13	380
qq	1321	TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 13	380
ò	1381	TCCTIGCATCCCCAGCTGGTCTGATCCCTGCCAGGCCCCTTCCTT	440
Dp	1381	TCCTTGCATCCCCAGCTGGTCTGATCCCTGCCAGGGCCCCTTCCTT	440
ò	1441	TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 15	500
qq	1441	TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 15	500
ò	1501	ACTCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTGGGGTAAT 15	560
Dp	1501	ACTCCATCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTCC	560
È	1561	TCAACAGTTAAAAGAAGCTTATTCTTAAATGTATTGTAT	620
Db	1561	TCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATT	620
ģ	1621	CTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTATCTTAACATGAC 16	680
Ор	1621		680
ò	1681	CACAGITIGIAAGIACTCGGCGGCGACCACGC 1713	
qq	1681	CACAGITITETAAGTACCTCGGCCGCGACCACC 1713	

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                                                                                              ATGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG
                                                                                                                                              CGGCCAACAGGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes human nucleic acid-associated proteins designated NAAP-1 to NAAP-57. The human NAAPs have cytostatic, antiatreriosclerotic, antiathergic, cerebroprotective, antiatherance antiparkinsonian, anticonvulsant, nootropic, neuroprotective, antiatiflammatory, ophthalmological, thyromimetic, antiarthritic, hepatotropic, antibacterial, virucide, protozoacide, antiparamitic and polymucleotide sequences can be used in gene therapy. The NAAP protein and polymucleotide sequences can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative diseases (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (Parkinson's disease, Alzheimer's disease, stroke, epilepsy), developmental disorders (renal tubular acidosis, anaemia, glaucoma, topic dermatitis, arthritis) antibilmamatory discorders (ADS, allergies, atopic dermatitis, arthritis) and infections (e.g. bacterial, viral, paramitic, protozoal, fungal). The present sequence encodes human NAAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human nucleic acid-associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
                                                                                                                                                                                                                   antiarteriosclerotic; anti-HIV; antialjergic; cerebroprotective; antiarteriosclerotic; anti-HIV; antialjergic; cerebroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; antiinflammatory; ophthalmological; thromimetic; antiarthritic; hepatotropic; antibacterial; virucide; protozoacide; antiparasitic; fungicide; gene therapy; cell proliferative disease; cancer; atherosclerosis; hepatitis; neurological disorder; Parkinson's disease; Alzheimer's disease; stroke; epilepsy; developmental disorder; renal tubular acidosis; anaemia; glaucoma; hypothyrcidism; autoimmune disorder; inflammatory disorder; AIDS; allergy; atopic dermatitis; arthritis; infection; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marquis JP;
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Burford N; Elliott VS, Emerling BM, Forsythe IJ, Gorvad AE, Griffin JA; Kable AE, Khare R, Lal PG, Lee EA, Lee SY, Li JX, Marquis C Rankumar J, Richardson TW, Sprague WW, Swarnakar A, Tang YT; Chawla NK, Warren BA, Yue H;
                                                                                                                                              Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98
                                                                                                                                                                                              human; nucleic acid-associated protein; NAAP; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; SEQ ID NO 98; 405pp; English
BP
ADD01260 standard; cDNA; 2392
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2002US-0347633P.
2002US-0351749P.
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                                                                                              (first entry)
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Ramkumar J, Richarαενω
'''' NK, Warren BA,
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25-JAN-2002;
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DB 10; Length 2392;

Score 1645; Pred. No. 0;

96.0%;

Query Match Best Local Similarity

Sequence 2392 BP; 471 A; 743 C; 674 G; 504 T; 0 U; 0 Other;

1215 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCCAGGAGACGACTGCAGATGCC

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ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC
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                                                                                                                                                                       TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGGCCATGGGATCTACATC
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                                TTCCAGGGCACCGACACACACTCGTCGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC
                                            TTCCAGGGCACCCGACACAGACTCGTCGGGGGCACCCTTGCTCCAGGGTGTACTGCTAACCC
                                                                             CTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGG
                                                                                          CTGCCAGGCCCAGCTGCCACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGG
                                                                                                                           GGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCC
                                                                                                                                                                                    TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGGCCATGGGATCTACATC
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tissue regeneration; cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
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The invention discloses a polymuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel

Crown 1970 fully defined nucleotide sequences which encode novel

Crown 1970 fully defined is a polympetide encoded by the polympetide or peptide or the polymucleotide, immunologically assaying the polympetide or peptide or the polymucleotide by contacting the polympetide or peptide or the encoded protein, and observing the binding between the two, a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide. The oligomucleotide is useful as a primer for synthesising the polymucleotide in an expressible manner and an antisense polymucleotide and encoded for detecting the polymucleotide. The oligomucleotide is useful as pharmaceutical agents and many disease-related correcting the polymucleotides and encoded correcting and be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of genes many be included in their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell

Cromedicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell

Cromedicines for regulated proteins, disease-related proteins and genes

Cromedicines are used as indicacrs for diseases (e.g. osteoporosis, encoding them can be used as indicacrs for diseases (e.g. osteoporosis, encoding them can be used as indicacrs for diseases (e.g. osteoporosis, encoding them can be used as indicacrs for consecutive or expression of the encoded protein to treat diseases. The cotivity or expression of the invention. Note: Some of the sequence cotivity or expression of the invention. Note: Some of the sequence cotivity or expression of the invention. Note: Some of the sequence of the sequence or the activity or expression of the invention of the cotivity or expression of the invention of the cotivity 
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1, Tamechika I;
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                                                                                                                                                                                                                                                                                      polynucleotides and polypeptides, useful for developing a diagnostic er or medicines for regulation of their expression and activity, or
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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                 05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
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Best Local Similarity 99.9
Matches 1694; Conservative
                                                                                                                                         i, Sugiyama T, B, J, Isono Y, H
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Yamamoto J,
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(DIAD-) DIADEXUS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
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mapping;

vulnerary; CNS-gen.; gene therapy; diagnostic; forensic;

DNA purification; procein purification; osteoparthritis; antiarthritic; osteopathic; musculoskeletal disease; osteoparosis; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy, Alabieimers disease; neuroprotective; nootropic; degeneration; parkinsons disease; antiparkinsonian; neurological disease; carebrovascular disease; acebroprotective; vasotropic; cardiovascular disease; autoimmune disease; immunosuppressive; immune disorder; viral infection; virucide; infection; cancer;

cytostatic; neoplasm; gene; ss

WO2005049806-A2 Homo sapiens.

02-JUN-2005

11-MAR-2004; 2004WO-US007412.

14-MAR-2003; 2003US-00389559

(NUVE-) NUVELO INC.

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New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral

infection, or cancer.

ä Y; Chen

Zhou P, Ma Goodrich R,

ъ, О, Ren I Wang I

Zhang J, Zhao Q,

Wang ZW, Asundi V,

Wang J, Xue A,

Boyle B;

Weng G,

Wehrman T, Tang TY, Ghosh M,

2005-417730/42.

P-PSDB; AEA20112

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The invention describes a new isolated polynuclectide (I) encoding a polypeptide with biological activity comprising: a nuclectide sequence of complete that by the polypeptide with biological activity comprising: a nuclectide sequence of (I) under stringent bybridization conditions; or a nuclectide sequence of (I) under stringent bybridization conditions; or a nuclectide sequence of (I). Also described are: a(I) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polymetide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 ([Mully defined), where the polypeptide of (S); a polymetide hybridiazing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3); a method carrier; an antibody directed against the polypeptide of (3); a method of polymolectide of (1); a method for identifying a compound that binds to the polypeptide of (3); a method of polymolectides, where the collection of (3); and a collection of polymolectides, where the collection of (3); and a collection of polymolectides, where the collection of (3); and a collection of polymolectides, where the collection of (3); and a collection of polymolectides, where the collection of (3); and a collection of polymolectides, where the collection of (3); and a collection of polymolectides, where the collection of (3); and activity, which comprises any of the amino acid sequences of SEQ ID NOS: 1-567. (I) is a polymuclectide comprising of activity, which comprises any of the amino acid sequences and methods are useful in the septimination; in destriction of methods are useful for treating a disease or disorders or compessition and method are useful for treating a disease, burns, CNS and peripheral disease, allaheimer's dependent on DNA and amino acid sequences. The composition and method are useful for treating a disease, burns, CNS and peripheral disorders,
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Sequence 791 BP; 149 A; 278 C; 222 G; 142 T; 0 U; 0 Other;

Query Match

Novel human polynucleotide SEQ ID NO 239.

(first entry)

11-AUG-2005

XXXXXX

**AEA19545** 

BP

AEA19545 standard; cDNA; 791

RESULT 6 **AEA19545**  39.9%; Score 683; DB 14; Length 791;

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                                                                                                                                                                                                                                                                                                                           The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the innormation, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                      New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
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100.0%; Pred. No. 3.5e-174;
iive 0; Mismatches 0;
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22-NOV-2000;
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The invention relates to a novel isolated nucleic acid molecule comprising: a sequence encoding a sequence comprising 11-1518 amino acids is a sequence comprising 190-8144 by; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides of the invention can be used to treat disorders by gene therapy. This polynucleotide represents a breast specific related sequence of the
                                                                                                                                                                                                                                                                                                         isolated nucleic acid molecule, useful for treating breast cancer, diagnosing or monitoring the presence of metastases of breast cancer
                            BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer; breast cancer; breast specific; human; ds.
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                                                                                                                                                                                                                                                  Liu
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Breast specific related polynucleotide SEQ ID No 104
                                                                                                                                                                                                                                                  Sun X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.1%; Score 3/8; 22.17;
100.0%; Pred. No. 8.2e-171;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                  Pluta
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                                                                                                                                                                                                                                                  Recipon
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                                                                                                                                                              21-NOV-2001; 2001WO-US043815.
                                                                                                                                                                                          22-NOV-2000; 2000US-0252509P.
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Matches 378; Conservative
                                                                                                                                                                                                                                                  Macina RA,
                                                                                                                                                                                                                     (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                            WPI; 2003-018927/01
                                                                                                    WO200277232-A2.
                                                                                                                                                                                                                                                                                                                                         in a patient
                            Cytostatic; metastatic;
                                                                                                                                 03-OCT-2002
                                                                                                                                                                                                                                                  Salceda S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCAGGAACCCCTGTGGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCTG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;
                                                                                                                                                                                                         Karra K,
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                                                                                                                                                                                                         Recipon H,
 gene therapy; cytostatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                               a coding sequence of the invention
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Liu C;
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Best Local Similarity
Matches 378; Conserval
                                                                                                                                                                          (DIAD-) DIADEXUS INC
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                                                         WO200264611-A1
                            Homo sapiens
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261 ACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTAT 320
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                                   201 GCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTG
                                                                     1045 ACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
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Pot D, Lamson (
, Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; gene therapy; colon cancer; prostate cancer; breast cancer; lung cancer; cancer detection; ss.
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Kassama A, Reinhard C, Randazzo F, Kennedy GC, "Pot D, Lam
Drmanac R, Crkenjakov Drmanac S, Dickson M, Labat I;
Leshkowitiz D, Kita D, Garcia V, Jones LW, Strache-Crain
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                                                                                                                                           1105 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCAT 1138
                                                                                                                                                              GGAGCTCCAGGGTACCCAGCAAGCCATGACTCAT 354
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99US-0142311P.
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
                                                                                                                                                           cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; 88.
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Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lam
Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
Leshkowitiz D, Kita D, Garcia V, Jones LW, Strache-Crain
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Pred. No. 1.1e-149;
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19.5%; Score 334; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 334; Conservative 0; Mismatches
                                                                                                                         Novel human polynucleotide, SEQ ID NO: 177.
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                 AAP64421 standard; cDNA; 393 BP.
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02-JUL-1999;
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                                                                                                                                                           Human; breast
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M. Brand B. B.

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                                                                                                                   140 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCACGAGCCGC 199
                                                                                                                                                                  200 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC 259
                                                                                                                                                                                                     TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTTCCGCCGGTGCCGGGATTGCCTCCAG 300
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                                                                                           CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC
                                                                                                                                           CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGATTACCTTC
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J, Innis MA, Garcia PD, Sudduth-Klinge
Randazzo F, Kennedy GC, Pot D. Kassam
Crkvenjakov R, Dickson M, Drmanac S, I
Garcia V, Jones WL, Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene expression product cDNA sequence SEQ ID NO:861
                     Indels
                                             1 ATGCCCCGCCCTGGACACCCCCCCCCCAGCATCTGGGCCTCCACGCT
          Pred. No. 2e-143;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                   CGCTGTGGAGCCTGTGTGCGG 400
                                                                                                                                                                                                                                                                                        CGCTGTGGAGCCTGTGTGCGG 321
100.08; 21.
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98US-0080114P.
98US-0080515P.
98US-0080666P.
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                     321; Conservative
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIRON CORP.
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           Similarity
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31-MAR-1998
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell conference of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides any also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1004
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Pred. No. 2.5e-133;
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100.0%; Pred. No. c...
'... 0; Mismatches
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Matches 300;
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241 CCGCTGCCCCCTGACAGTGGCCATGAGACCATGGTGGGCCCCAGGGTCTCAGCCAGGATG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New breast specific nucleic acids and proteins, useful for identifying,
                                                                                          980 CCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCAGCCAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, breast specific gene, breast specific protein, breast cancer, gene therapy, cytostatic, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing, monitoring, staging, imaging, and treating breast cance non-cancerous disease states in breast tissue, and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                             Human breast cancer associated coding sequence SEQ ID NO: 124
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100.0%; Pred. No. 7.4e-96;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                               BP.
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ID ABT07645 standard; cDNA; 654
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Matches 222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              14-NOV-2002
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                                                                                                                                                                                                                                                                                                              ABT07645;
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  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel isolated human polymucleotides obtained by screening for differential expression in colon cancer, breast cancer and lugared cancer call lines. The polymucleotides of the invention are represented in AAX98275-X99118 and encode polypeptides of protein captured in AAX98275-X99118 and encode polypeptides of protein capturities (AAA), eukaryotic aspartyl proteases, GATA family of callular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbolesters or diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, cyprotein thosphatase, trypsin, wnt family of developmental signalling proteins and WWY reps/WWP domain containing proteins. The encoded polypeptides also have a functional domain selected from Ank repeat, basis region plus leucine zipper transcription factors, bromodomain. EP-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (CCHC class), and zinc-binding metalloprotease domain. The polynucleotides encode polypeptides with similarity to known protein families and are predicted to have similar properties. The novel polynucleotides can be used to develop products for use as therapeutic agents and in forensic, genetic analysis, mapping and diagnostic applications. In particular, the product can be used for the detection and management of cancers. They can be used for treating e.g. cervical cancers, melanomas, colorectal adenocarcinomas, Nilm's tumour, sarcomas, cencers, melanomas, colorectal adenocarcinomas, leukemia, and any promyelocytic leukemia, monocytic leukemia, and management of cancers. They can be used for treating e.g. cervical cancers depatiary ectodermal dysplasia, of the cervix, fibrous dysplasia of the cervix, fibrous dysplasia of memary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast, be all the cervix, fibrous dysplasia of the cervix, fibrous dysplasia of the cervix, epithelial or thyroid hyperplasias or pseudoepithelial adrenal, breast, brin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCC 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                              Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCCAAGTGCACATCAGACACTG
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                                                                                                                                                                                                                                                                                                              Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                     D, Garcia PD, Suddutu-..-., Kennedy GC, Pot D, Kassam A. v.R, Dickson M, Drmanac S, La'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 249; DB 2; I
Pred. No. 7.9e-109;
                                                                                                                                                                                                                                                                                          Bacobedo J, Innie ... Kennedy c. Giese K, Randazzo F, Kennedy c. ....ac. R, Crkvenjakov R, Dicksor ....a V, Jones LW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 326; 591pp; English.
                                                                                                                98US-0080664P.
98US-0105234P.
98US-0105877P.
                                               98WO-US027610.
                                                                                            97US-0068755P
                                                                                                                                                                                         98US-00217471
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Local Similarity 99.7%;
les 299; Conservative
                                                                                                                                                                                                                                                                                                       Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                      CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-430243/36.
                                                                                                                                                                                                                                      (CHIR ) CHIRON COF
(HYSE-) HYSEQ INC.
                                             22-DEC-1998;
                                                                                            23-DEC-1997;
                                                                                                                   03-APR-1998;
21-OCT-1998;
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AAH69926/c
ID AAH699
XX
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1575 AAGCTTATCTTAAATGTATTGTATTGGGGGGTGGGCCAGGGCCCACTCTATGTTATGTTAA 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1635 GGAGITGGITCTGGITCTTGGCTGAIGITCTGTATCTTAACATGACCACAGITTGTAAGI 1694
                                                                                                                                                                                                                                                                                                                                                                                                                    of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AAGCTTATCTTAAATGTATTGTATTGGGGGGGGGGCAGGCCCACTCTATGTTATGTTAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for
treating lung
                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated human nucleic acid (I) encoding any
                                                                                                                  Human; gene therapy, vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene expression product cDNA sequence SEQ ID NO:4887.
                                                                                                                                                                                                                                                                                                                                           New isolated human nucleic acid molecule and polypeptide, identifying, diagnosing, monitoring, staging, imaging and cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 120 BP; 45 A; 33 C; 17 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 120; DB 6; I
llarity 100.0%; Pred. No. 7.6e-47;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                 Liu
                                                                                                                                                                                                                                                                                                 Sun X,
                                                                                               Lung specific nucleic acid (LSNA) #116.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 266; 389pp; English.
                                ABX92074 standard; cDNA; 120 BP
                                                                                                                                                                                                                                                                                                 Chen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ17414 standard; cDNA; 728 BP.
                                                                                                                                                                                                                                21-NOV-2001; 2001WO-US043612.
                                                                                                                                                                                                                                                      22-NOV-2000; 2000US-0252500P.
                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                 Macina RA, Recipon H,
                                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                     WPI; 2002-713376/77.
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Matches 120; Conserva
                                                                                                                                                                                     WO200268633-A2
                                                                                                                                                                Homo sapiens.
                                                                          08-MAY-2003
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                                                                                                                                                                                                            06-SEP-2002
                                                    ABX92074;
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         RESULT 15
ABX92074/c
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                                         원
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell cuspected of being cancerous, where the gene product is encoded by one of the S148 polynucleotides can be used as a source of primers and probes, which can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and charactering and to detect differences in expression levels between the conded protein); and to detect differences in expression levels between two calls (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic purposes. The polymorleotides of the invention are especially used in the cancer). The polymorleotides of the invention are especially used in the diagnosis, prognosis and management of colorects, cancer, and man and management of colorects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human genes and their expression products which are differentially expressed in different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones WL, Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sudduth-Klinger J;
                              detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
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Human; gene; gene expression product; diagnosis; therapy; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Garcia PD,
Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2%; Score 38; DB 2; Le
.00.0%; Pred. No. 1.9e-07;
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Best Local Similarity 100.0%; Pred. No. 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide analogues and antagonists
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98US-0075954P.
98US-0080114P.
98US-0080515P.
98US-0080666P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams LT, Escondur
Reinhard C, Giese K, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leshkowitz D, Kita D,
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                                                                                                                                 Homo sapiens
                                                                                                                                                                                               WO9938972-A2
                                                                                                                                                                                                                                                                                                                             28-JAN-1999;
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21-OCT-1998;
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New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is affilicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, ovarian cancer, identification, detection, characterisation, tumour, kinase, marker, cytostatic, antisense gene therapy, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 329 BP; 106 A; 45 C; 59 G; 119 T; 0 U; 0 Other;
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                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1686 TTTGTAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 TITGIAAGTACCTCGGCCGCGACCACGC
                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 226; 1051pp; English.
                                                                                                                                                                                              Berger A,
                08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MARA-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
09-UIM-2000; 2000US-0210600P.
21-UUL-2000; 2000US-021014P.
                990S-0169681P.
990S-0171350P.
2000US-0189315P.
2000US-0203791P.
2000US-0210600P.
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21-MAR-2000; 2000US-0191321P.
31-MAY-2000; 2000US-0208382P.
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AAF98612 standard; DNA; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001 (first entry)
                                                                                                                                                                                              Schlegel R, Deeds J,
                                                                                                                                                                                                                                   WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-211428/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
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                                                                                                                  Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
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Pred. No. 0.012;
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                                                                           Human cervical cancer marker nucleic acid 1200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker nucleic acid 712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 294; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH69438 standard; cDNA; 329 BP
                                                                                                                                                                                                                                                                                                            08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
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                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-375006/39
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                                                                                                                                                       Homo sapiens.
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                                    19-SEP-2001
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AAH69926;
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AAH69438

Query Match Matches

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08-DEC-1999;
21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
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                                             The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see ARPS9854 to ARPS98730), in a patient sample; and (2) the normal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (1) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used hybridoma, which produces an antibody useful for covarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAPS98573 to AAF98593 represent human kinase marker primers and probes which are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
 comprises detecting changes in the expression of a variety of markers.
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                                                                                                                                                                                                                                                          Score 26; DB 5; Length 91;
Pred. No. 0.11;
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                                                                                                                                                                                                                                   Sequence 91 BP; 23 A; 17 C; 20 G; 31 T; 0 U; 0 Other;
                                                                                                                                                                                                         in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker nucleic acid 1358.
                                                                                                                                                                                                                                                                   100.0%; Prea. ...
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                        Claim 1; Page 988; 1198pp; English
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21-DEC-1999; 99US-0171350P.
14-MAX-2000; 2000US-0189315P.
12-MAX-2000; 2000US-0203791P.
09-UUN-2000; 2000US-0210600P.
                                                                                                                                                                                                                                                                                                                                                                                                        AAH70084 standard; cDNA; 203
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Best Local Similarity 100.
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
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                                                                                                                     Length 203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cervical cancer marker nucleic acid 2181.
                                                                                                                     DB 4;
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100.0%; Pred. No. 0.11;
ive 0; Mismatches
                                                                        51 T; 0 U;
                                                                                                                                      100.0%; Prec. ...
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                                                                                                                     Score 26;
Pred. No.
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990S-0171350P.
2000US-0189315P.
2000US-0203791P.
                                                                          Sequence 203 BP; 52 A; 41 C;
                                                                                                                                                                                                                                                                                                                                                                               AAH70907 standard; cDNA; 412
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                                                                                                                        1.5%;
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Best Local Similarity luv...
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Matches 26; Conserv
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WO200257414-A2
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 Homo sapiens.
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                                       25-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                     invention
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ABV37465/
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                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising tracting and polypeptides are also useful for isolating compounds with cytostatic polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                                                                                                                                                                                                                                         New peptide useful as a marker for the diagnosis of breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 26; DB 4; Length 576;
.larity 100.0%; Pred. No. 0.11;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 576 BP; 134 A; 111 C; 125 G; 205 T; 0 U; 1 Other;
                                                                    Human breast cancer expressed polynucleotide 9868.
                                                                                       Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte derived cDNA SEQ ID NO 8473.
                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                  Wang Y, Steinmann K;
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       AAL17411 standard; cDNA; 576 BP
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24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193460P.
15-MAY-2000; 2000US-0205230P.
09-UNW-2000; 2000US-0211315P.
25-UUL-2000; 2000US-020534P.
                                                                                                                                                                         10-JAN-2001; 2001WO-US000798
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                                                (first entry)
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1e8 26; Conserv
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                                                                                                                                 WO200151628-A2.
                                                                                                             Homo sapiens
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                            AAL17411;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                Phillips J;
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Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec. ...
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                                                                                                                                                                                                                                K, Matcuk G, A
Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 26; Page 1920; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
22-OCT-2001; 2001WO-US047856.
                                                             20-OCT-2000; 2000US-0241994P.
08-JUN-2001; 2001US-0296764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV37465 standard; cDNA; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
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                                                                                                                                                                                                                             Wohlgemuth J, Fry K,
Ly N, Woodward R, Q.
                                                                                                                                                            (BIOC-) BIOCARDIA INC
                                                                                                                                                                                                                                                                                                                            WPI; 2002-636525/68.
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Homo sapiens
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                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV07533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV07533/
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                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; determining whether prostate cancer has metastasized in a patient; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 5; Length 255;
Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 255 BP; 56 A; 55 C; 80 G; 64 T; 0 U; 0 Other;
                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian cancer DNA marker #17410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 GTAAGTACCTCGGCCGCGACCACGC 73
                                                                                                                                                                                                               Claim 1; Page 7689; 11750pp; English.
                                                                                                 Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.5%; Scc
Local Similarity 100.0%; Pi
es 25; Conservative 0;
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AD143520/C

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AD143520;

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AD143520;

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C ADL43520;

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E Human ovarian cancer DNA marke

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Human; ovarian cancer; ds; tum

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Human; ovarian cancer; ds; tum

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Human; ovarian cancer; ds; tum

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Human; ovarian cancer; ds; tum

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YX

Human; ovarian cancer; ds; tum

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XX

YX

YX

YX

YX

Z1-SEP-2001;

XX

Z1-MAR-2001; 2001WG-US009126.

XX

Z1-MAR-2000; 2000US-0211940P.

PR

Z5-MAY-2000; 2000US-0211940P.

PR

Z5-MU-2000; 2000US-0211940P.

PR

Z5-MU-2000; 2000US-0211940P.

PR

Z5-MU-2000; 2000US-0211940P.

PR

Z1-DEC-2000; 2000US-0211940P.

PR

Z1-DEC-2000; 2000US-021661P.

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MILL-) MILLENNIUM PREDICTIVE |

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WPI; 2001-611502/70.
                         18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
            2000US-0211314P
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                                                                                                                            WPI; 2001-662795/76.
            09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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The invention relates to mucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the conference of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonucleotide complementary to a marker of the patient antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the expression levels indicates ovarian cancer. The level of expression of a sespense of a secreted protein or to a transcribed completed or its portion. The level of expression of the marker is a sessessed by detecting the presence in the sample, a protein or protein or protein crangement. Alternatively, the level of expression of the marker is assessed by detecting the marker, under stringent conditions. The polynucleotide which anneals with the marker or amneals with a portion of the marker is assessed by detecting the marker or amneals with a portion of the polynucleotide which anneals with the presence of a transcribed comprising the marker or amneals with a patient contained and an entire of expression of the marker is a subsequent contained and comparing the level of expression of the marker in a patient which involves detecting expression of the marker in a patient which involves detecting repeating the method at a subsequent contained and comparing the level of expression.
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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Pred. No. 0.34;
                                                                                                                                                                                          SEQ ID NO 17410; 106pp; English.
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16-MAR-2000; 2000US-0189862P.
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Matches 25; Conservative
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WO200170979-A2.
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                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer also metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
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                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                          assessing the aggressiveness or indolence of prostate cancer in a pat i (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                             Score 25; DB 5; Length 304; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                        Sequence 304 BP; 80 A; 63 C; 78 G; 76 T; 0 U; 7 Other;
                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                        1689 GTAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ovarian cancer DNA marker #11387.
                                                                                                                                                                                                                                                                                                                                                                                                            39 GTAAGTACCTCGGCCGCGACCACGC 15
                                                                                                                                                          Claim 1; Page 1214; 11750pp; English.
                                                                        Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL37497 standard; DNA; 310 BP
        09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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2000US-0220661P.
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                                                                                           WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lillie J;
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          09-JUN-2000;
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25-MAY-2000;
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                                                                       Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
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The invention relates to nucleic acid markers which are overexpressed in cancer cells as compared to their expression in normal (i.e. noncardan cancer cells as compared to their expression in normal (i.e. noncaded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the corded by the markers, antibodies that selectively bind to the corded by the markers of inhibiting ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing the level of expression of the amarker in a control non-ovarian cancer sample. A difference between the camerer corresponds to a secreted protein or to a transcribed to a secreted protein or to a transcribed corresponds to a secreted protein or to a transcribed corresponds to the marker. The level of expression of the marker corresponds to the marker. The level of expression of the assessed by detecting the presence in the sample, a protein or protein cragment corresponding to the marker. The presence of protein or protein cragment corresponding to the marker. The presence of protein or protein cragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker or anneals with a portion of the marker is also used for monitoring the presence of a transcribed out the polymucleotide which anneals with the marker or anneals with a portion of the marker is also used for monitoring the progression of ovarian cancer in a sample at a first point in time, repeating the method is carried out the sample at a first point in time, repeating the method is carried out sample and a first point in time, repeating the method of the marker of the printed specification, but was obtained in electronic format directly from winto int Amb/mhilahed no
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         ovarian
Novel isolated nucleic acid molecules (markers) overexpressed in ovaria cancer cells as compared to their normal non-cancerous ovarian cells ar used to characterize stage, grade, histological type of ovarian cancer.
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Pred. No. 0.34;
                                                                                                                                                                               Disclosure; SEQ ID NO 11387; 106pp; English.
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nes 25; Conservative
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Human; breast cancer; cell marker; cytostatic; ss.
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                                                                                                                                                                                                      29-MAR-2000;
15-MAY-2000;
                               Homo sapiens
                                                                                                                                                                                    24-MAR-2000;
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                                                                                          19-JUL-2001
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AAH69711/c
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                                                                                                                                                                                                                                                                       The invention relates to nucleic acid markers which are overexpressed in cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian calcs. The invention also relates to polypeptides canceded by the markers, antibodies that selectively bind to the collect opolypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclecide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer supplementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer supplementary to a marker of the marker in a patient sample and a normal level of expression of a marker orresponds to a secreted protein or to a transcribed of compression levels indicates ovarian cancer. The level of expression of the marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker or anneals with the protein or protein fragment. Alternatively, the level of expression of the marker is a slow used for monitoring the marker or anneals with a polynucleotide which anneals with the marker or anneals with a polynucleotide which anneals with the marker or anneals with a subsequent time and comparing the level of expression of the marker in a patient sample at a first point in time, repeating the method is carried out time and comparing the level of expression of the marker of the printed sample. A composition comprising the method of treat ovarian cancer polynerial speciment and many ovarian is also used the invention is used to
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                                                                                                                                                                                    Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
                                                                                                                                                                                                    cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer expressed polynucleotide 6865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.34;
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                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 5095; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1689 GTAAGTACCTCGGCCGCGACCACGC 1713
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           15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
25-JUL-2000; 2000US-0220661P.
                                                          2000US-0257672P
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                                                                                                                                                      WPI; 2001-611502/70.
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Best Local Similarity
                                                                                                                       Lillie J;
                                                          21-DEC-2000;
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The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide useful as a marker for the diagnosis of breast cancer.
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Pred. No. 0.34;
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21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
                                                                                                                                              2000US-0193480P.
2000US-0205230P.
2000US-0211315P.
                                                                                                               2000US-0192099P
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10-JAN-2001; 2001WO-US000798
                                                                                                                                                                                                                                     25-JUL-2000; 2000US-0220534P
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Best Local Similarity
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity (c) (a); or (f) degenerate variants of (a). Polypeptides (ABP68595-C) ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and propertides and proteins in the tumour colls, in vaccines and for gene colls exapt. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly content of the two the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acid markers which are overexpressed in
                                       SEQ ID NO 4393; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 453;
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Pred. No.
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2000US-0207124P.
2000US-0211940P.
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15-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL43881;
                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                     New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                              The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
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diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
cytostatic; tumour; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 359; 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 359 BP; 92 A; 57 C; 74 G; 135 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pancreatic cancer expressed cDNA SEQ ID NO 4393.
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                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.5%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 25; Conservative 0; Mismatches
                                                                                            Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1689 GTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                             Claim 1; Page 264; 1051pp; English
                                                                                              Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lodes MJ,
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2001US-0305484P.
2001US-0313999P.
09-JUN-2000; 2000US-0210600P
21-JUL-2000; 2000US-0220114P
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2001US-0267568P.
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                                                                                                                                                                                                                                                                                                                                                                                                         useful for gene therapy
                                                                                            Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Benson DR, Kalos MD,
                                                                                                                                  WPI; 2001-375006/39
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                                                                                            Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2002
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cancerous) ovarian cells as compared to their expression in normal (i.e. noncarcerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides corcesponding to a marker antibodies that selectively bind to the corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a complement corresponds to a secreted protein or to a transcribed polymucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein cragment corresponding to the marker. The presence of protein or protein cragment is detected using an antibody that specifically binds with the protein or protein cragment. Alternatively, the level of expression of the marker is a sessessed by detecting the presence of a transcribed comprising the marker or anneals with a portion of the polymucleotide comprising the marker, under stringent conditions. The patient which involves deferent in a pration of the marker in a pration of the patient which involves deference the marker in a pration of the polymucleotide comprising the marker, under stringent conditions. The patient which involves deference the marker in a pration of the patient which involves deference the marker in a protein or protein or protein or protein or protein or protein or protein or protein or protein or protein or protein or protein or protein or protein or protein or p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form at directly the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast specific, cancer staging, cancer imaging, breast cancer, non-cancerous disease states in breast tissue; gene therapy, vaccine;
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100.0%; Pred. No. 0.34;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recipon H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS67274 standard; cDNA; 810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic animal; gene; ss.
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Sun Y;
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Best Local (
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Liu C,
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ABS67274/c
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                                                                                                                                             The invention describes a breast specific nucleic acid. The nucleic acids, polypeptides, antibodies, agonists and antagonists, and compositions comprising them are useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and noncancerous disease states in breast tissue, in gene therapy, vaccine development, in producing transpenic animals and cells, and in producing engineered breast tissue for treatment and research. The nucleic acids may be used as molecular markers for detecting breast cancer for accurate staging of the disease and monitoring the progress of cancer treatments, and as hybridisation probes or primers. This sequence encodes a breast specific protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention as exptostatic. The antibody is useful for electection perfectly in the detection of breast tumours. (I) is useful an invention are useful in the detection of breast tumours. (I) is useful an arker for breast cancer and in breast cancer therapy. Sequences given
                                                        cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
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                                                        diagnosing, monitoring, staging, imaging, and treating breast canc
non-cancerous disease states in breast tissue, or for gene therapy
                                    New breast specific nucleic acids and proteins, for identifying,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer; breast; tumour; cytostatic; marker; detection; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 810 BP; 216 A; 183 C; 145 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                 Claim 1; Page 156; 227pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 25; Conservative
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WPI; 2002-657590/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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ABT23431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel method for monitoring differential expression of genes in a filamentous fungal cell. Specifically, it refers to identifying differential gene expression occurring between two related filamentous fungal cells and comprises adding detection reporter labeled nucleic acids of filamentous fungal cells to a substrate array of trichoderma resea; (T. resea;) expressed sequenced tagg (ESPs), or suppression subtractive hybridization (SSH) clones and detecting a signal in the array. The present invention further describes a computer readable of the array. The present invention further describes a computer readable of in the array. The present invention further describes a computer readable of in the array. The present invention further describes a computer readable of the first filamentous fungal cells. It also provides a search in one or more second filamentous fungal cells. It also provides a search of the comparing a target sequence (s). Accordingly, it provides a contifer sequence (s). Accordingly, it provides a computer conting the homologous sequence(s). Accordingly, it provides a microorganism is grown on cellulose or corn stover, as well as for discovering new genes, identifying possible functions of unknown open cending frames and monitoring gene copy number variation and stability.

Note that this method utilizes an array where one spot equals one gene or open reading frame, which makes extensive follow-up characterization con unnecessary since sequence information is available and EST and/or SSH
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in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T_reesei suppressive subtractive hybridization (SSH) cDNA clone Seq 1051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monitoring differential expression of genes of two filamentous fungal cells, for e.g. discovering new genes, comprises adding labeled nucleic acids to an array of Trichoderma reesei expressed sequenced tags and
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression; suppressive subtractive hybridization; microarray;
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                                                                                                              Sequence 1252 BP; 269 A; 229 C; 238 G; 336 T; 0 U; 180 Other;
                                                                                                                                                       1.5%; Score 25; DB 11; Length 1252; 100.0%; Pred. No. 0.34; ative 0; Mismatches 0; Indels
                                                                       site at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                 1689 GTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                      224 GTAAGTACCTCGGCCGCGACCACGC 200
                                                                                                                                                                                                                                                                                                                                                                                                    ADY99697 standard; cDNA; 150 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVOZYMES BIOTECH INC.
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                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypocrea jecorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microorganism; ss.
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The invention relates to an isolated polymucleotide which encodes an immune related protein or a protein exhibiting biological properties of an immune-related protein as sequence selected from 26 sequences. The expression vector and reagent are useful for the preparation of a capture such as allergic, autoimmune, inflammancry or infectious diseases, such as allergic, autoimmune, inflammancry or infectious diseases, e.g. asthma, allergic rhinitis, atopic dermatitis, hives, conjunctivitis, systemic lupus erythematosus, myasthenia gravis, sepsis, sepsis, gout, or colitis. The polypeptides may at the encine of activity, as a bait protein in a two-hybrid or three-hybrid assay to identify other proteins which bind to or interact with the human immune-related protein and modulate its activity, and for immunisation of mammals. The polynucleotides of the invention can
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microarrays can be organized based on function of the gene products. This polymuclectide sequence is a T. reses! SSH cDNA clone that forms part of the substrate array of the invention. NOTE: The SeqIDS 1-1188 referring to T. reses! ESTs or SSH clones or their combinations are available in electronic form from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antiallergic; antiinflammatory; antiasthmatic; dermatological; ophthalmological; immunosuppressive; immune related; allergic; autoimmune; inflammatory; infectious disease; asthma; allergic rhinitis; atopic dermatitis; hives; conjunctivitis; systemic lupus erythematosus; myasthenia gravis; psoriasis; sepsis; gout; colitis; immunisation; gene therapy; mouse; murine; ds.
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                                                                                                                                                                                                                                        (http://seqdata.uspto.gov/sequence.html; Document ID:20050069934)
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1.44; occidents 1, 188; occidents 1, 198; Pred. No. 1;
Best Local Similarity 100.04; Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the
be used in gene therapy for treating disorders. This sequence represents an immune-related mouse protein of the invention. This polynucleotide represents an immune-related mouse DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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...ve 0; Mismatches
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Best Local Similarity 100.'
Matches 24; Conservative
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25-JUL-2000;
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                 the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method at a subsequent using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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protein fragment. Alternatively, the level of expression of
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tive 0; Mismatches
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25-MAY-2000; 2000US-027124P.
15-UTN-2000; 2000US-0211940P.
07-UTL-2000; 2000US-0216820P.
25-UTL-2000; 2000US-022661P.
21-DEC-2000; 2000US-0257672P.
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                                                                                                                                                                                                                                                                      using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
with ovarian cancer, which involves comparing the level of expression of an arxier in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a
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invention. The markers are useful for assessing if a patient is afflicted
with ovarian cancer, which involves comparing the level of expression of
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corresponding the marker, under stringent conditions. The
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2000US-0211940P.
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2000US-0220661P.
2000US-0257672P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL42505 standard; DNA; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2000;
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21-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001.
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70. Lillie J;

Lee J,

21-MAR-2001; 2001WO-US009126

2000US-0211940P 2000US-0216820P.

25-JUL-2000; 2000US-0220661P. 21-DEC-2000; 2000US-0257672P.

07-JUL-2000;

21-MAR-2000; 15-JUN-2000;

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concernus) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of trating a patient antisense oligonuclectide complementary to a marker of the patient an antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the cancer in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed comparing to the marker. The presence of protein or protein cancer is assessed by detecting the presence in the sample, a protein or protein or protein or protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprised by detecting the presence of a transcribed protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed collecting the presence of a transcribed collecting the progression of the marker in a portion of the marker. In a portion of the marker in a signal with the marker, under stringent conditions. In a marker in a portion of the marker in a signal with the marker in a portion of the marker in a portion of the marker in a parting the progression of the marker in a portion of the marker in a paint of expression of the marker in a portion of the marker in a paint of expression of the marker in a paint of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                        Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 283 BP; 94 A; 62 C; 50 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                Disclosure; SEQ ID NO 16395; 106pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
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Best Local Similarity
                                                     WPI; 2001-611502/70.
Lillie J;
Lee J,
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancer) ovarian cancer cells as compared to their expression in normal (i.e. noncancer) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cancer inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention. The patient and antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a control non-ovarian cancer. The level of expression of the carpression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed cassessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed corresponding to the marker. The presence of a transcribed corresponding to the marker. The presence of a transcribed corresponding to the marker is approximent in a patient which anneals with the marker or anneals with a portion of the marker is also used for monitoring the presence or anneals with a portion of patient which involves detecting expression of the marker in a patient or protein in the sample at a first point in time, repeating the method at a subsequent corresponds the level of expression of covarian cancer in a patient wing an ovarian tissue sample. A composition comprising a marker, or mainsonder and an enable of the marker is also used for monitoring the reserved or time and comparing the level of expression of constitution or time and comparing the invention is used to retar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide or antibody of the invention is used to treat ovarian this sequence represents a human ovarian cancer DNA marker of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 310 BP; 72 A; 54 C; 66 G; 118 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 3678; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 24; DB 100.0%; Pred. No. 1; Live 0; Mismatches
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Best Local Similarity 100.0
Matches 24; Conservative
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ID ADI772
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ADL36491 standard; DNA; 312 BP

ADL36491/c RESULT 43

20-MAY-2004

ADL36491;

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covarian caneer cells as compared to their expression in normal (i.e. non-
covarian caneer cells as compared to their expression in normal (i.e. non-
cancerous) ovarian cells. The invention also relates to polypeptides
encoded by the markers, antibodies that selectively bind to the
corded by the markers, antibodies that selectively bind to the
encoded by the markers, antibodies that selectively bind to the
corresponding ovarian cancer involving inhibiting expression of a gene
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
marker in a patient sample and a normal level of expression of the
a marker in a patient sample and a normal level of expression of the
corresponds to a secreted protein or to a transcribed
polynuclectide or its portion. The level of expression of the arker in a patient and an earker. The presence of protein or protein
fragment corresponding to the marker. The presence of protein or protein
fragment corresponding to the marker. The presence of a transcribed
polynuclectide or its portion. The level of expression of the arker is a sessessed by detecting the presence of a transcribed
polynuclectide which anneals with the marker or anneals with a portion of
the polynuclectide which anneals with the marker or anneals with a potion of
the polynuclectide which anneals with the marker or anneals with a potion of
the polynuclectide which anneals with the marker or anneals with a protein or patient
sample at a first point in time, repeating the method at a subsequent
cusing an ovarian tissue sample. A composition comprising a marker,
companing the level of expression of the marker of the
sample or antibody of the invention is used to treat ovarian cancer.
This sequence represents a human ovarian cancer DNA marker or the printed appendication, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to nucleic acid markers which are overexpressed in
                        Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 9991; 106pp; English.
                                                                                                                                                                                                                                                    ; 2000US-0191031P.
; 2000US-0207124P.
; 2000US-0211940P.
; 2000US-0216820P.
; 2000US-0220661P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee J, Lillie J;
                                                                                                               WO200170979-A2
                                                                      Homo sapiens.
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DB 5; Length 310; 100.0%; Pred. No. -; Score 24; Local Similarity Query Match Best Loca Matches

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Gaps ö

0; Indels

24; Conservative

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1690 TAAGTACCTCGGCCGCGACCACGC 1713
                          30 TAAGTACCTCGGCCGCGACCACGC
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides canced by the markers, antibodies that selectively bind to the canced by the markers, antibodies that selectively bind to the parient of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclecide complementary to a marker of the invention. The markers are useful for assessing the level of expression of the amarker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the carrier portion or ovarian cancer ample. A difference between the marker corresponds to a secreted protein or to a transcribed of polynuclectide or its portion. The level of expression of the marker corresponds to a secreted protein or to a transcribed polynuclectide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein cragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker or anneals with a portion of polynuclectide comprising the marker or anneals with a portion of the polynuclectide comprising the marker or anneals with a patient colynuclectide which anneals with the marker or anneals with a patient content which involves detecting the progression of the marker in a patient consider a first point in time, repeating the method is carried out time and comparing the level of expression. The method is carried out cuing an ovarian tissue sample. A composition cancer in a patient detected the invention is need to treat ovarian cancer. This sequence represents a human ovarian cancer plant and an a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                           Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                               Human ovarian cancer DNA marker #10381
                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207124P.
2000US-0211940P.
2000US-0216820P.
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21-DEC-2000; 2000US-0257672P
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                                                                                                                                                                                                                       Homo sapiens.
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RESULT 45
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ID ADI7
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                                                                  Length 312;
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                                 Seguence 312 BP; 99 A; 53 C; 47 G; 113 T; 0 U; 0 Other;
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches
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                                                                                                                                      1690 TAAGTACCTCGGCCGCGACCACGC 1713
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25-MAY-2000; 2000US-0207124P.
15-UIN-2000; 2000US-0211840P.
07-UUL-2000; 2000US-0216820P.
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21-DEC-2000; 2000US-0257672P.
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polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method at a subsequent using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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100.0%; Pred. No. 1;
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2000US-0211940P.
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Best Local Similarity 100.
Matches 24; Conservative
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07-JUL-2000;
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marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein or fragment is detected using an antibody that specifically binds with the fragment or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, mile and ovarian tissue sample. A composition of the marker in a patient which involves detecting expression. The method is carried out using an ovarian tissue sample. A composition comparising an earker.
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100.0%; Pred. No. 1;
tive 0; Mismatches 0; Indels
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ses 24; Conservative
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concoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense objected complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the capters ovarian cancer. The level of expression of a marker oversponds to a secreted protein or to a transcribed expression bevels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed corresponding to the marker. The presence of protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed or the pulynucleotide which anneals with the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a patient or marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient or sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression of the marker is also used for monitoring the pressure or the proprising a marker. The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the propriet or first point in the sequence date for this patent did not form part of the printed specification, but and a s
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genetic analysis; diagnostic; antisense therapy; gene; ss.
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from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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ative 0; Mismatches
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Best Local Similarity 100.
Matches 24; Conservative
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Thiaglingam A, Lewis ME;
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covarian cancer cells as compared to their expression in normal (i.e. noncerous) ovarian cells. The invention also relates to polypeptides encoded by the marker, antibodies that selectively bind to the cenceded by the marker, antibodies that selectively bind to the cenced by the marker of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprishing providing to cells of the patient an antisense oligomuclectide complementary to a marker of the invention. The marker is a patient sample and a normal level of expression of the arker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of the carrier corresponding to the level of expression of the carrier corresponding to the marker. The presence of protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide of or monitoring the presence of a transcribed or marker is assessed by detecting the presence of a transcribed or marker is assessed by detecting the marker or anneals with a pottion of the polynucleotide which anneals with the marker or anneals with a pottion of the polynucleotide comprising the marker or anneals with a patient or protein that the level of expression of the marker in a patient which involves detecting the presence of a transcribed or antibody of the invention. The method is carried out time and comparing the level of expression or the printed specification, but was obtained in all and or form part 
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100.0%; Pred. No. 1.
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21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-021051P.
09-UUN-2000; 2000US-0210600P.
21-UUL-2000; 2000US-02210600P.
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ID AAH69655 standard; cDNA; 331
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Best Local Similarity 100.(
Matches 24, Conservative
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                                                                                                  ABQ563106 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60775 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of colon cancer in a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate acrossors on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acid markers which are overexpressed in
      tissues useful for determining the presence of colon cancer in a cell tissue type, and in antisense therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 320 BP; 66 A; 89 C; 89 G; 75 T; 0 U; 1 Other;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 TAAGTACCTCGGCCGCGACCACGC 312
                                                                 Claim 1; Fig 1; 796pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL44057 standard; DNA; 326 BP
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2000US-0216820P.
2000US-0220661P.
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Matches 24; Conserv
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Length 326; 0; Indels

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potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
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14-MAR-2000; 2000US-0189315P-
12-MAR-2000; 2000US-0203791P-
09-JUN-2000; 2000US-0210600P-
21-JUL-2000; 2000US-0220114P-
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                                                                                                 24; Conservative
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                                                                                     Local Similarity
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Matches
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AAH69708/
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                                                New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                      cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                           genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                           100.0%; Pred. No. 1;
tive 0; Mismatches
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 Zhao X;
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.00.0%; Pred. No.
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                                                                                   Claim 1; Page 257-258; 1051pp; English
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 Berger A,
                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                           The invention relates to novel
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24 'MAR-2000; 2000US-0192099P:
29-MAR-2000; 2000US-0192099P:
15-MAY-2000; 2000US-026330P:
09-JUN-2000; 2000US-0211315P:
                                                                                                                                                                                                                                                                                                                                                                                        AAL13080 standard; cDNA; 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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 Deeds J,
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                      WPI; 2001-375006/39.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200151628-A2.
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 Schlegel R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-mailgnant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                               Gape
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                                                            DB 4; Length 337;
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Pred. No. 1;
0; Mismatches 0; Indels
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Sequence 337 BP; 127 A; 63 C; 60 G; 83 T; 0 U; 4 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cervical cancer marker nucleic acid 982.
                                                            1.4%; Score 24; DB
100.0%; Pred. No. 1;
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                         Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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live 0; Mismatches
                                                                                   Human prostate expression marker cDNA 7995
                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 24;
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                   ABV08004 standard; cDNA; 346 BP
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2000US-0211314P.
2000US-0219007P.
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                                                              (first entry)
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Best Local Similarity 100.
Matches 24; Conservative
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                                                                                                                                                               WO200160860-A2
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09-JUN-2000;
18-JUL-2000;
                                                                                                                                           Homo sapiens.
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                                                               13-SEP-2002
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                                          ABV08004;
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          ABV08004/c
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancercuus) ovarian calls. The invention also relates to polypeptides cancercuus) ovarian calls. The invention also relates to polypeptides cancercuus) ovarian cancer intibodies that selectively bind to the at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves complementary to a marker of the patient an antisense oligonuclectide complementary to a marker of the patient an apatient sample and a normal level of expression of a marker in a patient sample and a normal level of expression of expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynuclectide or its portion. The level of expression of the marker corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the from the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comparising the marker, under stringent conditions. The marker is as suesded for monitoring the presence of a transcribed comparising the level of expression of the marker in a patient correct in a patient which involves detecting the presence of a transcribed comparising the level of expression of the marker is a subsequent correction of the marker is a subsequent correction of the marker or anneals with a pocifically binds and comparish the level of expression of the marker is a subsequent correction of the marker is a bound for marker in a patient which involves detecting the presence of a transcribed or marker is also used for monitori
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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25-MAY-2000; 2000US-0207124P.
15-JUN-2000; 2000US-021940P.
07-JUL-2000; 2000US-0216820P.
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The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a the patient afflicted with ovarian cancer comparising providing to cells of the patient an antiense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer useful for assessing if a patient the afflicted with ovarian cancer sample. A difference between the carrier or a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed cor its portion. 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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of
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marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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consider corresponds to a secreted protein or to a transcribed polymucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein or protein or protein or protein or protein or protein or protein or protein or protein or protein fragment. Alternatively, the level of expression of protein or protein fragment. Alternatively, the level of expression of marker is assessed by detecting the presence of a transcribed polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method at subsequent using an ovarian tissue sample. A composition comprising a marker, colling and ovarian tissue sample. A composition comprising a marker. This sequence represents a human ovarian cancer DNA marker of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, ss.
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                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 24;
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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Best Local Similarity 100.0
Matches 24, Conservative
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25-MAY-2000;
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progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has mecastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a
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                                                                                                                                                                                                                5; Length 376;
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                                                                                                                                                                          Sequence 376 BP; 122 A; 55 C; 63 G; 136 T; 0 U; 0 Other;
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ive 0; Mismatches
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Pred. No.
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2000US-0211940P.
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Best Local Similarity 100.'
Matches 24; Conservative
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15-JUN-2000;
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cc marker corresponds to a secreted protein or to a transcribed
cc polynucleotide or its portion. The level of expression of the marker is
cc sasessed by detecting the presence in the sample, a protein or protein
c fragment corresponding to the marker. The presence of protein or protein
cc fragment is detected using an antibody that specifically binds with the
cc protein or protein fragment. Alternatively, the level of expression of
the marker is assessed by detecting the presence of a transcribed
cc the polynucleotide comprising the marker or anneals with a portion of
cm polynucleotide comprising the marker under stringent conditions. The
cc marker is also used for monitoring the progression of ovarian cancer in a
cc patient which involves detecting expression of the marker in a patient
cc sample at a first point in time, repeating the method at a subsequent
cc time and comparing the level of expression. The method is carried out
cusing an ovarian tissue sample. A composition comprising a marker,
cc polypeptide or antibody of the invention is used to treat ovarian cancer.
cc This sequence represents a human ovarian cancer DNA marker of the
contribution. Note: The sequence data for this patent did not form part of
c from with a fre wind int was obtained in electronic format directly
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100.0%; Pred. No. 1;
:ive 0; Mismatches
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coroded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk cof developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the invention. The patient is apatient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or transcribed polynuclectide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynuclectide which anneals with the marker or anneals with a portion of the polynuclectide comprising the marker, under stringent conditions. The patient which involves detecting expression of the marker in a patient cancer in a patient sample at a first point in time, respecting the method at a subsequent cancer in a contain and comparing the level of expression.
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100.0%; Pred. No. 1;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the printed specification, but was obtained in electro
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian cancer DNA marker #2902.
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2000US-0207124P.
2000US-0211940P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200170979-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncarrian cancer cells as compared to their expression in normal (i.e. noncancerus) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cancer intibodies that selectively bind to the encoded by the markers and inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a captient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the captession levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed complement is detected using the presence in the sample, a protein or protein fragment or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is assessed by detecting the presence of a transcribed content or protein fragment is assessed by detecting the presence of a transcribed content or protein fragment is assessed by detecting the presence of a transcribed content or protein fragment is assessed by detecting the presence of a transcribed content or protein fragment is assessed by detecting the marker or anneals with a portion of the polymucleotide which anneals with the marker is a second for monitoring the presence or anneals with a portion of marker is a let used.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
                                        Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are
                                                                                      used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
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100.0%; Pred. No. ..
                                                                                                                                 Disclosure; SEQ ID NO 2902; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian cancer DNA marker #16375.
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25-MAY-2000; 2000US-0207124P.
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ID ADL42485 standard; DNA; 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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us-09-989-890-105.oligo.rng

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancrous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cancer antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide companiementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sample. A difference between the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of marker corresponds to a secreted protein or a transcribed marker in a solution. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that sample, a protein or protein fragment is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of grotein or protein or protein an antibody that specifically binds with the protein or protein assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of the marker is assessed by detecting the presence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
27-JUL-2000; 2000US-025061P.
21-DEC-2000; 2000US-0257672P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611502/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lillie J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee J,
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

Disclosure; SEQ ID NO 9592; 106pp; English.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70.

Lee J, Lillie J;

2000US-0207124P. 2000US-0211940P.

2000US-0216820P 2000US-0220661P

21-DEC-2000; 2000US-0257672P

21-MAR-2001; 2001WO-US009126

21-MAR-2000; 15-JUN-2000; 07-JUL-2000; 25-MAY-2000;

WO200170979-A2 Homo sapiens.

27-SEP-2001

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of the invention. The marker in a patient sample and a normal level of expression of a marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of a compared or secreted protein or to a transcribed polymucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the polymucleotide doming to the marker. The presence of a transcribed polymucleotide which anneals with the marker of a subsequent conditions. The marker is also used for monitoring the presence of a transcribed of the marker is also used for monitoring the presence of a transcribed of marker is also used for monitoring expression of the marker is a subsequent tissue sample. A composition comparising a marker of this an ovarian cancer in a patient which involves detecting expression. The method at a subsequent using an ovarian tissue sample. A composition comparising a marker of the invention is used to transcribed out invention.
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Matches 24; Conserv
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ADI70525/c
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tive 0; Mismatches
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Best Local Similarity
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ADI76850;

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Matches

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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                  Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3267; 106pp; English
                                                                                    Human ovarian cancer DNA marker #3267.
Mon Mar 13 12:24:32 2006
                                                                                                                                                                                   2000US-0207124P.
2000US-0211940P.
2000US-0216820P.
                                                                                                                                                             21-MAR-2001; 2001WO-US009126
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                                                                                                                                                                                                                21-DEC-2000; 2000US-0257672P
                                                                                                                                                                                                          2000US-0220661P
                                       ADI70525 standard; DNA; 392
                                                                     (first entry)
                                                                                                                                                                                                                                                             WPI; 2001-611502/70.
                                                                                                                                                                                                                                              Lillie J;
                                                                                                                                WO200170979-A2
                                                                                                                  Homo sapiens.
                                                                                                                                                                                          1S-JUN-2000;
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                                                                     20-MAY-2004
                                                                                                                                              27-SEP-2001
                                                      ADI70525
                                                                                                                                                                                                                                              Lee J,
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The intention retailed as compared to their expression in normal (i.e. noncancerous) ovarian cells. The invention also relates to polypeptides
cancerous) ovarian cells. The invention also relates to polypeptides
canceded by the markers, antibodies that selectively bind to the
polypeptides, a method of inhibiting ovarian cancer in a patient at risk
of developing ovarian cancer involving inhibiting expression of a gene
corresponding to a marker of the invention and a method of treating a
patient afflicted with ovarian cancer comprising providing to calls of
the patient an antisense oligonuclectide complementary to a marker of the
invention. The markers are useful for assessing if a patient is afflicted
with ovarian cancer, which involves comparing the level of expression of
a marker in a control non-ovarian cancer. The level of expression of the
marker corresponds to a secreted protein or to a transcribed
control non-ovarian cancer. The level of expression of a
marker corresponds to a secreted protein or to a transcribed
control or its portion. The level of expression of the marker is
assessed by detecting the presence in the sample, a protein or protein
fragment corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker, the presence of expression of the
protein or protein fragment. Alternatively, the level of expression of
the marker is assessed by detecting the presence of a transcribed
corresponding to the marker is positically binds with the
protein or protein fragment. Alternatively, the level of expression of
the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent using an ovarian tissue sample. A composition comprising a marker, bolypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. The invention relates to nucleic acid markers which are overexpressed in

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Sequence 392 BP; 115 A; 50 C; 78 G; 146 T; 0 U; 3 Other;
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                                                                                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, useful
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Length 392;
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 DB 5;
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                100.0%; Pred. No. 1; ive 0; Mismatches
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   1.4%; Score 24;
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                                                                                  30 TAAGTACCTCGGCCGCGACCACGC
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16-MAR-2000; 2000US-0189652P.
25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-0211314P.
18-UUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                               ABV08052 standard; cDNA; 404
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                                   24; Conservative
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nes 24; Conserv
Query Match
Best Local Similarity
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Sequence 409 BP; 124 A; 85 C; 90 G; 110 T; 0 U; 0 Other;

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncaarerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides canceded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and method of treating a patient afflicted with ovarian cancer comparing providing to cells of the patient an antisense oligonocleotide complementary to a marker of the patient an antisense oligonocleotide complementary to a marker of the patient an antisense oligonocleotide comparing the level of expression of the marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed cancer sample and a normal level of expression of the marker corresponds to a secreted protein or to a transcribed cassessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is also used for monitoring the presence of a transcribed collymucleotide which annothed an entance and patient which involves detecting expression of the marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker is also used for monitoring the progression of the arker of oplypeptide or antibody of the invention. The method is carried out time and comparing the level of expression. The method is carried out the painted specification, but was obtained in electronic format direction.
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ADL42159 standard; DNA; 409 BP
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25-JUL-2000; 2000US-0220661P.
21-DEC-2000; 2000US-0257672P.
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2000US-0211940P.
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15-JUN-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerums) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers that selectively bind to the encoded by the markers to the invention and method of treating a corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the expression levels indicates ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed comprised by detecting the presence in the sample, a protein or protein or fragment is detected using an antibody that specifically binds with the fragment is detected using an antibody that specifically binds with the protein or protein fragment is detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the marker is assessed by detecting the presence of a transcribed the polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide which ameals with the marker or anneals with a portion or protein pragardance.
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5; Length 409;
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Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 1; Matches 24; Conservative 0; Mismatches
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                                                                                              1690 TAAGTACCTCGGCGGGCCACGC 1713
                                                                                                                          ADL43269 standard; DNA; 415 BP
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2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
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25-JUL-2000;
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ADL43269/
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marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 1;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                             Sequence 415 BP; 140 A; 73 C; 92 G; 110 T; 0 U; 0 Other;
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2000US-0207124P.
2000US-0211940P.
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Best Local Similarity 100.
Matches 24; Conservative
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07-JUL-2000;
25-JUL-2000;
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expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed marker is portion. The level of expression of a assessed by detecting the presence in the sample, a protein or protein corresponding to the marker. The presence of protein or protein cragment corresponding to the marker. The presence of protein or protein cragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprising the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient cample at a first point in time, repeating the method at a subsequent cusing an ovarian tissue sample. A composition comprising a marker. This sequence represents a human ovarian cancer DNA marker of the
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Pred. No. 1;
0; Mismatches
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100.0%; Pred.
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Best Local Similarity 100.
Matches 24; Conservative
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25-JUL-2000;
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15-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                  invention.
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ADI72479/c
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WPI; 2001-611502/70.

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cc encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of the carbers in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a carbers orresponds to a secreted protein or a transcribed corpy, assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the corporation or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed copy, uncleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The carber is also used for monitoring the presence of a transcribed copy, and the level of expression of the marker in a patient corresponding and an antibody that progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient confined and comparing the level of expression of the marker in a patient confined and comparing the level of expression of the marker or anneals with the composition comprising a marker or anneals with a portion of patient which involves detecting expression of the marker in a subsequent confined or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer in a patient of the marker or an anneal subsequent confined and comparing the method is carried out the sequence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 1.4%; Score 24; DB 5; Length 416; l. Similarity 100.0%; Pred. No. 1; 24; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0211940P.
2000US-0216820P.
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Best Local Similarity
Matches 24; Conserv
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15-JUN-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian calcs. The invention also relates to polypeptides canceded by the markers, antibodies that selectively bind to the canceded by the markers, antibodies that selectively bind to the patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sumple. A difference between the amarker in a patient sample and a normal level of expression of a marker corresponds to a secreted protein or to a transcribed corresponds to a secreted protein or to a transcribed corresponds to a secreted protein or to a transcribed oplynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker. The presence of polynucleotide which anneals with the marker or anneals with a sportion of the polynucleotide comprising the marker; under stringent conditions. The marker is also used for monitoring the progression of fovarian cancer in a polynucleotide which anneals with the marker or anneals with a specient which involves detecting expression of the marker in a pubsequent time and comparing the level of expression of the marker in a subsequent cuing an ovarian tissue sample at a first point in time, repeating the method is carried out time and comparing the level of expression of the marker in a subsequent cuing an ovarian tissue sample. A composition comprising a new part of invention. Note: The sequence represents a human ovarian cancer DNA marker of the printed part into a represente
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                                       Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the printed specification, but was obtained in electron from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                   Disclosure; SEQ ID NO 12779; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.0%; Pred. No. 1; tes 24; Conservative 0; Mismatches
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                         cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
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                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                       2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
                    2000US-0207124P
                                                                                                          21-DEC-2000; 2000US-0257672P
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Best Local Similarity
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                                       15-JUN-2000;
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                    25-MAY-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncaded by the markers, antibodies that selectively bind to the cancerous) ovarian cells. The invention also relates to polypeptides canceded by the markers, antibodies that selectively bind to the canced by the markers, antibodies that selectively bind to the cancer cancerous) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an enters which involves comparing the level of expression of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer. Which involves comparing the level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer sample. A difference between the expression of the marker in a control non-ovarian cancer sample, a protein or protein cassessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that sample, a protein or protein fragment is detected using an antibody that sample, a protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comparising the anxier or annestibed an antibody that aspecifically binds with the copyunclectide which annested with the marker or annested out the polymuclectide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of the marker is also used for monitoring the progression of the marker is also used for monitoring the progression of the marker of the polymoclectide which annessed by the expression of the marker of the polymoclectide which annessed by the expression of the marker of the polymoclectide which annessed by the expression of the marker of the printed speci
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nes 24; Conserv
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                                                                      WO200170979-A2
Homo sapiens.
                                                                                                                                                                                                                                                                                              21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2000;
                                                                                                                                                                                                                                                                                                                                     25-MAY-2000;
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Matches
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ABV39230/

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Breast cancer related marker, seq id 7580.
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                                                                                                                                                                                                                                      18-JUL-2001; 2001US-0306220P.
                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001WO-US005171
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                                                                                                                                                                                                                                                                                                                                              WPI; 2003-787014/74.
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                                                                                         Homo sapiens
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                                                                                                                                                             29-MAY-2003
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                                                                                                                                                                                                                                                                                                          Lillie J,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastisat in a patient; determining whether prostate cancer has metastisat in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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1;
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                                                                                                                                                                                Human prostate expression marker cDNA 39221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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100.0%; Pred. No. 1;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
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                                                                      ABV39230 standard; cDNA; 424 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
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                                                                                                                                          (first entry)
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nes 24; Conservative
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25-MAY-2000;
09-JUN-2000;
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                                                                                                        ABV39230;
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(first entry)

02-DEC-2004

ACN86430/C ID ACN86 XX AC ACN86 XX DT 02-DE

RESULT 73

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Best Loc Matches

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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleocide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention are useful in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACNYB81-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 425 BP; 136 A; 92 C; 90 G; 106 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 7580; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Xu Y, Wang Y, Steinmann K;
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Novel isolated nucleic acid molecules (markers) overexpressed in cancer cells as compared to their normal non-cancerous ovarian ce
  WPI; 2001-611502/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h)
                                                                                                                                                                                                                                                                                                                               assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB 5; Length 426;
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 426 BP; 116 A; 102 C; 110 G; 98 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian cancer DNA marker #18496
                                                                                                                                                                                       Claim 1; Page 1075; 11750pp; English.
                                                                                             Monahan JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 TAAGTACCTCGGCCGCGACCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL44606 standard; DNA; 426 BP
             2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                              2000US-0255281P
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2000US-0220661P.
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                                                                                            Schlegel R, Endege WO,
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16-MAR-2000; 25-MAY-2000; 209-JUN-2000;
                                                13-DEC-2000;
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                                    18-JUL-2000;
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ADL44606/c
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncarcance) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient afflicted with ovarian cancer complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a control non-ovarian cancer. The level of expression of the capression levels indicates ovarian cancer. The level of expression of a marker ourseponds to a secreted protein or to a transcribed capression of the marker corresponds to a secreted protein or to a transcribed corresponds to the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is detected using the marker. The level of expression of the marker is assessed by detecting the presence of a transcribed corresponding the marker or anneals with the marker or anneals with the marker or anneals with the marker or anneals with a portion of patient which involves detecting expression of the marker in a patient or protein fragment is detected for monitoring the presence of a transcribed caption and comparing the level of expression of the marker is also used for monitoring the presence of a transcribed out the polymeledial or a first point in time, repeating the marker or anneals with a partient or protein or protein or protein or protein or protein or protein or protein or protein or protein or
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cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 37916.
                                                                                                      Disclosure; SEQ ID NO 18496; 106pp; English.
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Mismatches
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Best Local Similarity 100.
Matches 24; Conservative
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
  WPI; 2001-611502/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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Matches
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                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h)
                                                                                                                                                                                                                                                                                                                               assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                    prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    ch 1.4%; Score 24; DB 5; Length 432; 1. Similarity 100.0%; Pred. No. 1; 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                Sequence 432 BP; 153 A; 67 C; 75 G; 137 T; 0 U; 0 Other;
                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian cancer DNA marker #18622.
                                                                                                                                                                                                                                                                                                                                                                                                                                    1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                      Claim 1; Page 7755; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S6 TAAGTACCTCGGCCGCGACCACGC 33
                                                                                             Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL44732 standard; DNA; 432 BP
2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0207124P.
                                    2000US-0219007P
                                               13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001WO-US009126.
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                                                                                             Endege
                                                                                                                  WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200170979-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2000;
                        09-JUN-2000;
                                    18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-2000;
                                                                                           Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL44732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADL44732/c
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 77
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancercous) ovarian cells. The invention also relates to polypeptides cancercous) ovarian cells. The invention also relates to polypeptides cancercus) ovarian cancer intolving a selectively bind to the coorded by the markers, antibodies that selectively bind to the gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a patient afflicted with ovarian cancer involving inhibiting expression of the patient an antisense oligonucleotide complementary to a marker of the patient an antisense oligonucleotide complementary to a marker of the patient and a normal level of expression of the invention. The marker is a patient sample and a normal level of expression of the arker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of a marker corresponds to a secreted protein or to a transcribed comprision of the marker is assessed by detecting the presence of protein or protein fragment is postion. The level of expression of the marker is assessed by detecting the presence of protein or protein fragment is assessed by detecting the presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of protein comprising the presence of protein or protein fragment. Alternatively, the level of expression of the marker is an antibody of the presence of comparing the level of expression of the marker is a seessed by detecting expression of the marker in a patient time and comparing the level of expression of ovarian cancer in a patient which involves detecting expression of the marker is an ovarian cancer in a patient of expression of ovarian cancer 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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Disclosure; SEQ ID NO 18622; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1690 TAAGTACCTCGGCCGCGACCACGC 1713
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100.0%; Pic
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25-MAY-2000; 2000US-0207124P.
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the amarkers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the amarker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a corresponds to a secreted procein or to a transcribed polymucleotide or its portion. The level of expression of a gasessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the fragment is detected using an antibody that specifically binds with the corresponding to the marker. The level of expression of the marker is assessed by detecting the presence of a transcribed to polymucleotide which anneals with the marker or anneals with a portion of marker is also used for monitoring the presence or anneals with a portion of polymerer is a leaver of the polymerestion of formanian proving the presence or anneals with a portion of polymerer is a leaver of the marker is also need to the marker is also need to a marker is a leaver of the polymerestion of formanian proving the presence of a transcribed to expression of the polymerestion or proving the presence of a transcribed to expression of the polymerestic the polymerestic the polymerestic the polymerestic the
The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concernation articles that selectively bind to the concernation of a gene corresponding to a marker of the invention and a method of inhibiting ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antilesness objoincleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker or corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein ciragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprised of the marker, under stringent conditions. The marker is also used for monitoring the presence of a transcribed comprised the marker, under stringent conditions. The marker, which is an antibody that specifically binds with a partient or protein in an antibody that specifically binds with the marker is also used for monitoring the progression of ovarian cancer in a marker in a partient and a marker.
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                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovarian tissue sample. A composition comprising a marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 437 BP; 102 A; 88 C; 91 G; 150 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide or antibody of the invention is used
                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3100; 106pp; English
                              2000US-0216820P
                                                                 25-JUL-2000; 2000US-0220661P.
21-DEC-2000; 2000US-0257672P.
                                                                                                                                                                                                                                                                                                                          WPI; 2001-611502/70.
                                                                                                                                                                                                                                                 Lillie J;
                                  07-JUL-2000;
                                                                                                                                                                                                                                                     Lee J,
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70. Lillie J;

Lee J,

21-DEC-2000; 2000US-0257672P

07-JUL-2000; 25-JUL-2000; 15-JUN-2000; 25-MAY-2000;

2000US-0207124P. 2000US-0211940P. 2000US-0216820P. 2000US-0220661P.

21-MAR-2001; 2001WO-US009126

WO200170979-A2.

27-SEP-2001

Disclosure; SEQ ID NO 9426; 106pp; English.

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marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the lovel of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%; Pred. No. 1; local Similarity 00.0%; Pred. No. 1; Pred. Section 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred. No. 1; pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

Homo gapiens

Human ovarian cancer DNA marker #9426.

(first entry)

20-MAY-2004 ADI76684;

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Gaps

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0; Indels

100.0%; Pred. ...

Conservative

Local Similarity les 24; Conserv

Best Loc Matches

Query Match

1690 TAAGTACCTCGGCCGCGACCACGC 1713

30 TAAGTACCTCGGCCGCGACCACGC

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BP

ADI76684/c ID ADI76684 standard; DNA; 437

1.4%; Score 24; DB 5; Length 437;

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1690 TAAGTACCTCGGCCGCGACCACGC 1713

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concerous) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antilesnes oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the carresponds to a patient sample and a normal level of expression of the carresponds to a secreted protein or to a transcribed complementary corresponds to a secreted protein or to a transcribed polymucleotide or its portion. The level of expression of a sessessed by detecting the presence in the sample, a protein or protein crangement is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprised by detecting the presence of a transcribed configuration the marker is assessed by detecting the presence of a transcribed comprised by detecting the presence of a transcribed marker is a species of monitoring the progression of a praison of the marker is a species of protein or protein or protein and the particles of the marker in a particle of the protein or protein or protein or protein or protein or protein detected using an antibody that species of protein or protein or protein dete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to treat ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a human ovarian cancer DNA marker of the
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                                                                                                                                                                                                                       Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                        Human ovarian cancer DNA marker #18016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0207124P.
2000US-0211940P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000US-0216820P.
25-JUL-2000; 2000US-0220661P.
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This sequence represents a
20-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200170979-A2
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancer cells as compared to their expression in normal (i.e. non-cancer cells of the invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides cencoded by the markers, antibodies that selectively bind to the conception of a gene corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the patient afflicted with ovarian cancer, which involves comparising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assession of the arker in a control non-ovarian cancer. The level of expression of the marker in a control non-ovarian cancer. The level of expression of the captession levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed comportion to portein or protein or protein or protein or protein fragment corresponding to the marker. The presence of protein or protein or fragment is detected using an antibody that specifically binds with the corresponding the marker, under stringent conditions. The polymucleotide which anneals with the marker or anneals with a portion or the polymucleotide which anneals with the marker or anneals with a patient or protein fragment. Alternatively, the level of expression of the marker is also used for monitoring the presence or anneals with a patient or patient which involves detecting expression of the marker in a patient or sample at a fifst point in time, repeating the method at a subsequent cime and comparing the level of expression. The method is carried out time and comparing the level of expression the period or treat ovarian cancer. Colling an ovarian tissue sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                             Human ovarian cancer DNA marker #15845.
           83
106 TAAGTACCTCGGCCGCGACCACGC
                                                                                                                          ADL41955 standard; DNA; 444 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0191031P.
2000US-0207124P.
2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee J, Lillie J;
                                                                                                                                                                                                                                                                                                                                                                                              WO200170979-A2
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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15-JUN-2000;
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25-JUL-2000;
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                                                                             RESULT 81
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Gaps

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Query Match 1.4%; Score 24; DB 5; Length 442; Best Local Similarity 100.0%; Pred. No. 1; Matches 24; Conservative 0; Mismatches 0; Indels

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Mismatches

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Conservative

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1690 TAAGTACCTCGGCCGCGACCACGC 1713
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 Matches
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This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                Human, prostate cancer, cytostatic; carcinogen, pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                           Gaps
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                                                                                 DB 5; Length 444;
1;
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1;
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                                                          Sequence 444 BP; 152 A; 77 C; 116 G; 99 T; 0 U; 0 Other;
                                    from WIPO at ftp.wipo.int/pub/published pct sequences.
                                                                           1.4%; Scor.
100.0%; Pred. No. .,
... 0; Mismatches
                                                                                                                                                                                                                                                                                           Human prostate expression marker cDNA 36032.
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                                                                                                                                 1690 TAAGTACCTCGGCGGGGCCACGC 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                                                                                                                 73 TAAGTACCTCGGCCGCGACCACGC
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2000US-0219007P.
                                                                                                                                                                                                                    ABV36041 standard; cDNA; 446
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                                                                                                                                                                                                                                                                   (first entry)
                                                                                                           24; Conservative
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                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            WO200160860-A2
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18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                        Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                     Human prostate expression marker cDNA 37963.
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100.0%; Pred. No. 1;
+ive 0; Mismatches
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                 78
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101 TAAGTACCTCGGCCGCGACCACGC
                                                                                                                                                               BP.
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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ID ABV37972 standard; çDNA; 446
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Best Local Similarity
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09-JUN-2000;
18-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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ABV45101/c

100.0%; Pred. No.

2000US-0191031P

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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 10610; 106pp; English
                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                              25-MAY-2000; 2000US-0207124P.
15-UTN-2000; 2000US-0211940P.
07-UTL-2000; 2000US-0216820P.
25-UTL-2000; 2000US-025066LP.
21-DEC-2000; 2000US-0257672P.
                                                                                         21-MAR-2001; 2001WO-US009126
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                                                                                                                                                                                                                                   Lee J, Lillie J;
                                       WO200170979-A2
                Homo sapiens.
                                                                                                                 21-MAR-2000;
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ADI71564/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate cancer in a patient
                                                                                                  Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                             Human prostate expression marker cDNA 45092.
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ABV45101 standard; cDNA; 446 BP
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25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
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                                                                                                                                           Homo sapiens.
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                                                   16-SEP-2002
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides cancerous) ovarian cancer antibodies that a selectively bind to the encoded by the markers, antibodies that a selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonuclecide complementary to a marker of the invention. The marker is a patient sample and a normal level of expression of the invention. The marker in a patient sample and a normal level of expression of a marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the marker in a patient of a secreted protein or to a transcribed polynuclectide or its portion. The level of expression of the marker is a session of the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the polynuclectide which anneals with the marker, under stringent conditions. The marker is also used for monitoring the presence of a transcribed patient which involves detecting expression of the marker in a patient cancer in a patient which involves detecting expression of the marker in a patient cancer in a gubsequence of a unit and compariant shall be level of expression of the marker in a patient cancer in a guangle at a first point in time, repeating the method as a subsequence of uning an ovarian cancer in a patient which involves detecting the involvence repression of the invention is used to treat ovarian cancer. This 
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100.0%; Pred. No. 1;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acid markers which are overexpressed in
                                                                                                                                                                                                                                                                                                                                         Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                             Human ovarian cancer DNA marker #4306.
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15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
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21-DEC-2000; 2000US-0257672P.
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This sequence represents a
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ADI71564;
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1.4%; Score 24; DB 5; Length 446; 100.0%; Pred. No. 1;

Query Match Best Local Similarity

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Human, nootropic, neuroprotective, cytostatic, dermatological, virucide, immunosuppressive, antiinflammatory, anti-HIV; antibacterial, vulnerary, antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebective, antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal, antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
                                                                                                                                Human nervous system related polynucleotide SEQ ID NO 135.
1690 TAAGTACCTCGGCGCGCGCCACGC 1713
              30 TAAGTACCTCGGCCGCGACCACGC
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2000US-0218290P.
2000US-0220963P.
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2000US-0225270P.
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                                                                    ABA11128 standard; cDNA; 449
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2000US-0229509P.
2000US-0229513P.
2000US-0230437P.
2000US-0231242P.
2000US-0231244P.
2000US-0231414P.
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13-0CT-2000;
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20-0CT-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins

(ABB14678-ABB18001) useful for preventing, treating or ameliorating

medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant) agonists are useful in

the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

covarian cancer and other cancers of the adrenal gland, bone, bone marrow,

breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

disorders e.g. Addison's disease, allergies, autoimmune haemolytic

anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease,

multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

cardiovascular disorders such as myocardial ischaemias; (d) wound healing

cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f)

infections diseases eugh as viral, bacterrial, fungal and parasitic

infections. Note: The sequence data for this patent did not form part of

the printed specification, but was obtained in electronic format directly

crome with the printed specification in the patences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
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ative 0; Mismatches
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                            2000US-0249218P-
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2000US-024929P-
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2000US-0259391P-
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ID ABQ75327 standard; cDNA; 457 |

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DT 05-NOV-2002 (first entry)
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2000US-0251868P.
2000US-0251869P.
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2000US-0254097P
                                                                                                                                                                                                                                                                                                                             2000US-0251989P
                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-541565/60.
P-PSDB; ABB14802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                            17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                   05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                   17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
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08-DEC-2000;
11-DEC-2000;
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The present invention describes an isolated lung specific nucleic acid (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid sequences comprising 17 - 733 amino acids, given in ABP22873 to ABB2285; (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b), comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific protein (LSP) sequences have cytostatic activity and can be used in gene therapy and vaccines. LSNAs and LSPs are useful for diagnosing and monitoring the presence and metastases of lung cancer in a patient. An entibody that specifically binds to an LSP can be used for determining the presence of an LSP in a sample, as well as for treating a patient with lung cancer, particularly by inducing an immune response against the lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs and LSPs are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer (e.g. squamous cell carcinoma) and noncancerous disease states in lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                      New lung specific nucleic acid useful in gene therapy or as vaccines for treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung diseases, as well as for diagnosing, monitoring or staging these
                                                   Human, lung, lung specific nucleic acid; LSNA; lung specific protein; LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer; squamous cell carcinoma; gene; chromosome 8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 6; Length 457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 457 BP; 163 A; 70 C; 100 G; 124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
               Human lung specific nucleic acid sequence SEQ ID NO:66.
                                                                                                                                                                                                                                                                                                                                                                Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 2.,
100.0%; Pred. No. 1;
Five 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian cancer DNA marker #18705.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 186; 282pp; English.
                                                                                                                                                                                                                                                                                                                                                                Chen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL44815 standard; DNA; 460 BP.
                                                                                                                                                                                                                                               20-NOV-2001; 2001WO-US045080.
                                                                                                                                                                                                                                                                                   20-NOV-2000; 2000US-0252054P.
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                                                                                                                                                                                                                                                                                                                                                                Macina RA, Recipon H,
                                                                                                                                                                                                                                                                                                                          (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-657601/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                     WO200264788-A2
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                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                           22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL44815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70. Lee J, Lillie J;

21-DEC-2000; 2000US-0257672P

2000US-0211940P.

25-MAY-2000; 15-JUN-2000; 07-JUL-2000; 25-JUL-2000:

2000US-0191031P

21-MAR-2000;

21-MAR-2001; 2001WO-US009126

27-SEP-2001

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerums) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concernum ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient at risk or patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker in a control non-ovarian cancer. The level of expression of a careful cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a gesessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed completed which anneals with the marker or anneals with the protein cross assessed by detecting the presence of a transcribed polynucleotide comprising the presence of a transcribed completed the marker. In a portion of the marker is assessed by detecting the presence of a transcribed completed the marker is assessed by detecting the presence of a transcribed completed the marker is assessed by detecting the presence of a transcribed completed the marker is assessed by detecting the presence of a transcribed completed the marker is a second or anneals with the marker in a portion of the polynucleotide comprising the progression of the profession of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 18705; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; Pred. No. 1; es 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24;
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ID ACN8
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70. Lee J, Lillie J;

2000US-0207124P. 2000US-0211940P. 2000US-0216820P.

25-MAY-2000; 15-JUN-2000; 07-JUL-2000; 25-JUL-2000;

25-JUL-2000; 2000US-0220661P 21-DEC-2000; 2000US-0257672P

us-09-989-890-105.oligo.rng

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                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN7881-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.thml?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                   Novel isolated polypeptide associated with breast cancer, useful for
                                                                                                                                                                                                                                                                                                                                 detecting presence of polypeptide in sample, as a marker for breast
                                                                            Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 463 BP; 105 A; 124 C; 116 G; 109 T; 0 U; 9 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. .,
                                                                                                                                                                                                                                                                                                                                                                         Disclosure, SEQ ID NO 5501; 36pp; English.
                                                    Breast cancer related marker, seq id 5501
                                                                                                                                                                                                                                                                Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4%; Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ovarian cancer DNA marker #3344.
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ID AD170602/C

XX

AC AD170602;

XX

CO-MAY-2004 (first entry)

XX

DE Human ovarian cancer DNA marker #

XX

KW Human; ovarian cancer; ds; tumour

XX

CO-MAY-2004 (first entry)

XX

CO-MAY-2004 (first entry)

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CO-MAY-2004 (first entry)

XX

CO-MAY-2004 (first entry)

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CO-MAY-2004 (first entry)

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CO-MAY-2004 (first entry)

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CO-MAY-2004 (first entry)

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CO-MAY-2004 (first entry)

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PD 27-SEP-2001.

XX

Z1-MAR-2001; 2001WO-US009126.
                                                                                                                                                                                   18-JUL-2002; 2002US-00198846.
                                                                                                                                                                                                            18-JUL-2001; 2001US-0306220P.
                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
                                                                                                                                                                                                                                                                                         WPI; 2003-787014/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                               Lillie J, Xu Y,
                                                                                                                               US2003099974-A1.
                          02-DEC-2004
                                                                                                                                                         29-MAY-2003
 ACN84351;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncarancerous) ovarian calls. The invention also relates to polypeptides cancerous) ovarian calls. The invention also relates to polypeptides cancoded by the markers, antibodies that selectively bind to the a trisk corresponding to a marker of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to amarker of the invention and a method of treating a patient afflicted with ovarian cancer comprishing providing to calls of the patient an antisense oligomuclectide complementary to a marker of the patient an autisense oligomuclectide complementary to a marker of the marker in a patient sample and a normal level of expression of a marker in a patient sample and a normal level of expression of expression levels indicates ovarian cancer. The level of expression of a marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a complament corresponds to a secreted protein or to a transcribed for marker corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the fragment is assessed by detecting the presence of a transcribed comprising the marker, under stringent conditions. The patient which involves detecting expression of the marker in a patient construction in time, repeating the method at a subsequent construction of the presence of a transcribed comparing the level of expression of the marker in a patient construction of the involves detecting expression of the marker in a patient construction of the marker is a subsequence of protein or protein in time, repeating the method at a subsequence conjuriant such conjuriation of the involves detecting expression of the marker is also used for monitoring the presence of protein or protein or protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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100.0%; Pred. No. 1,
... 0; Mismatches
Disclosure; SEQ ID NO 3344; 106pp; English.
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ID AD17/

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ADL41961 standard; DNA; 471 BP

RESULT 93 ADL41961/ ADL41961;

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the encoded by the markers antibodies that selectively bind to the train of the polypeptides, a method of inhibiting ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the arker orresponds to a secreted protein or to a transcribed cappers or assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the fragment is detected using an antibody that specifically binds with the corresponding to the marker. The level of expression of the marker is assessed by detecting the presence of a transcribed complyanced by detecting the presence of a transcribed complyanced by detecting the marker or anneals with a portion of the marker is assessed by detecting the marker or anneals with a portion of the polynucleotide which anneals with the marker is a same or marker in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a patient in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                     2000US-0207124P.
2000US-0211940P.
2000US-0216820P.
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21-DEC-2000; 2000US-0257672P.
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                                                                                                             WO200170979-A2
                                                            Homo sapiens.
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15-JUN-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the corresponding to a marker of the invention and method of treating a corresponding to a marker of the invention and method of treating a corresponding to a marker of the invention and method of treating a corresponding to a marker oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the amarker in a control non-ovarian cancer sample. A difference between the corresponds to a secreted protein or to a transcribed cassessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the corresponding to the marker. The level of expression of fragment is detected using an antibody that specifically binds with the corresponding to the marker. The level of expression of the marker is assessed by detecting the presence of protein or protein or protein fragment is detected using an antibody that specifically binds with the corresponding to morphy the presence of a transcribed control fragment is assessed by detecting the marker or anneals with a portion of the polynucleotide which anneals with the marker is assessed by detecting the marker, under stranscribed case the polynucleotide comparising the marker is an an antibody that specifically detection or protein or protein fragment. The level of expression of the polynucleotide comparising the marker is an animal to a marker is a len used for morphy and an animal and an animal and an animal and an animal and an animal and an animal and an animal and an animal and an animal and an animal and an animal and an animal and animal 
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                                                                                                          Human ovarian cancer DNA marker #15851.
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concerous) ovarian cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of tracting a patient afflicted with ovarian cancer complementary to a marker of the invention and a method of tracting a patient afflicted with ovarian cancer comparising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer. The level of expression of the expression ladicates ovarian cancer. The level of expression of a cancer corresponds to a secreted protein or to a transcribed cassessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is assessed by detecting the presence of a transcribed conting which anneals with the marker or anneals with a portion of
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                                                      DB 5; Length 471;
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               Sequence 471 BP; 132 A; 68 C; 104 G; 167 T; 0 U; 0 Other;
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                                                   Ouery Match
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches
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                                                                                                                               1690 TAAGTACCTCGGCCGCGACCACGC 1713
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the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                              Sequence 486 BP; 177 A; 69 C; 86 G; 135 T; 0 U; 19 Other;
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marker in a control non-overlan cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient sample at a first point in time, respeating the marker in a patient cample at a first point in time, respeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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marker in a patient sample and a normal level of expression of the
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21-DEC-1999; 99US-0171350P.
14-MAR-2000, 2000US-018911SP.
12-MAY-2000; 2000US-021391P.
09-JUN-2000; 2000US-0210600P.
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The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the necoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sample. A difference between the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed arker is assessed by detecting the presence in the sample, a protein or protein
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cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
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                                                                                                                      Sequence 500 BP; 145 A; 108 C; 99 G; 148 T; 0 U; 0 Other;
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                                                                                                                                                            1.4%; Score 24; DB 100.0%; Pred. No. 1; tive 0; Mismatches
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15-UN-2000; 2000US-0211940P.
07-UUL-2000; 2000US-0216940P.
25-UUL-2000; 2000US-025061P.
21-DEC-2000; 2000US-0257672P.
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fragment corresponding to the marker. The presence of protein or protein cragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide comprising the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of covarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, colypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                  rom WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0211940P.
2000US-0216820P.
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15-JUN-2000;
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corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the can marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker is corresponds to a secreted protein or to a transcribed comparing the presence in the sample, a protein or protein of protein or protein corresponding to the marker. The presence of protein or protein craspending to the marker. The presence of a transcribed of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprising the marker, under stringent conditions. The polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The patient which involves detecting expression of the marker in a patient or patient which involves detecting expression for the marker in a patient cample at a first point in time, repeating the marker in a subsequence time and comparing the level of expression. The method at a subsequence time and comparing the level of expression comprising a marker.

Colympetide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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25-JUL-2000; 2000US-0220661P
21-DEC-2000; 2000US-0257672P
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are

WPI; 2001-611502/70.

Lillie J;

Lee J,

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

21-DEC-2000; 2000US-0257672P

used to characterize stage, grade, histological type of ovarian cancer.

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covarian canacea to nucleic acid markers which are overexpressed in cancerous) ovarian cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the cancerous) ovarian cancer involves cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer involves complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer mapped of expression of the marker corresponds to a secreted protein or to a transcribed compounding the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the polymucleotide which anneals with the marker or anneals with a portein or protein or protein fragment is detected using the marker, under stringent conditions. The polymucleotide which anneals with the marker or anneals with a postence of a transcribed comprising the marker or anneals with a presence of a transcribed compounded for monitoring the prosession of the marker is also used for monitoring the prosession of a cancer in a patient which involves detecting expression of the marker is a first point in time, repeating the marker in a patient comparing the invention is used to treat ovarian cancer in a patient which involves demercing expression of the marker of the polymeted or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer of the polymeted or antibody of the invention is used to treat o
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                                                                 invention relates to nucleic acid markers which are overexpressed in
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                   Disclosure; SEQ ID NO 4993; 106pp; English.
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ADL41725 standard; DNA; 521 BP.
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07-JUL-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides canced by the markers, antibodies that selectively bind to the concoded by the markers antibodies that selectively bind to the patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense obligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sumple. A difference between the amarker in a patient sample and a normal level of expression of a marker in a control non-ovarian cancer. The level of expression of a marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or a transcribed corresponds to a secreted protein or a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient comparing the level of expression of ovarian cancer in a patient time and comparing the level of expression of the marker is a special ovarian tissue sample. A composition comprising a marker of the cusing an ovarian tissue sample. A composition comprising a marker of the sequence represente a human ovarian cancer DNA marker of the control of the prince of presence of patient of an enemal such of the prince of patient of an enemal such of the prince of the prince of pat
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38         24         1.4         394         8         CV888266         AW681360           390         24         1.4         395         1         AW681360         CB707964           391         24         1.4         400         8         CV971920         CB707964           392         24         1.4         400         8         CV971920         CB707964           393         24         1.4         403         6         CF063579         CB707964           394         24         1.4         403         6         CF063579         CB707964           395         24         1.4         408         6         CB70404         CB704074           396         24         1.4         408         6         CB70404         CB704074           397         24         1.4         408         6         CB704074         CB770407           396         24         1.4         408         6         CB704074         CB770407           397         24         1.4         414         7         CN042166         CR0432166           400         24         1.4         417         6         CF049280	24 1.4 446 8 CX94413B CX94413B 24 1.4 446 8 CX94413B 24 1.4 447 8 CY972905 24 1.4 447 9 1 AL725932 24 1.4 456 7 CV99694 24 1.4 457 7 CO499694 24 1.4 457 7 CO499794 24 1.4 457 6 CR73580B 24 1.4 464 6 CR73580B 24 1.4 468 6 CR73580B 24 1.4 468 6 CR73580B 24 1.4 468 6 CR73580B 24 1.4 469 6 CR73580B 24 1.4 469 6 CR73580B 24 1.4 469 6 CR73580B 24 1.4 469 6 CR73580B 24 1.4 471 8 DN97634B 24 1.4 471 8 DN97634B 24 1.4 477 6 CR72634B 24 1.4 476 7 CO497907 24 1.4 476 7 CO497907 24 1.4 477 6 CR72634B 24 1.4 477 6 CR72634B 24 1.4 477 6 CR72634B 24 1.4 476 7 CO497907 24 1.4 476 7 CO497907 24 1.4 476 7 CO497907	35         24         1.4         478         6         CF054863         CF054863           36         24         1.4         479         1         AL728170         AL728170           37         24         1.4         480         1         AL731033         AL731033           39         24         1.4         481         6         CD975018         CV972956           41         24         1.4         481         6         CD972956         CV972956           41         24         1.4         482         5         BQ739259         CV972956           43         24         1.4         485         6         CA726268         CV972956           44         24         1.4         485         6         CA726268         CV972956           44         24         1.4         485         6         CA726268         CV972956           45         24         1.4         487         1         AL719441         AL719441           45         1.4         488         1         AL719441         AL719441           46         2.4         1.4         488         1         AL719441           47 </td			

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Homo sapiens FLJ34633 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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I (bases I to 1197)
Nieleen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., Mhite,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1246 AAGCAGTGCCACTCTGGCTCCTGCCTTGGCTGGGTTCCTGGACCATGGCTT
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   CCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGA
                                                            CAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGAT
                                                                                                               CTCCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGG
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                                         CAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGAT
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                                                                      /organism="Homo sapiens"
//organism="Homo sapiens"
//db xref="taxon:9606"
/clone="DKFZp668B17277"
/tissue type="prostate"
/clone="Dip="686 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfilA + SfilB"
//dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MPRPGHPRPASGPPRLGPWERPTELCLETYDKPPQPPPSRRTRR
PPDKOPGHPGPESITFISSARBALESPTCLLETPLRGLLFWTGPRSTWBCPPLIVH
PPAGGWASGSSQPWAAASATPMLSSKRSLCTPTRGPPPQPLWRTPARSHWPIPHPCD
TACRAPLPVVLVAPRSTILSMSRTWTCRRWAVAPCRABKLMCSSSRS"
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 18
Further information about the clone and the sequencing project available at http://mips.gsf.de/projects/cdna/. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      /codon_start=1
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/db_xref="G1:51476785"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.5%; Score 1361; D
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                     /gene="DKFZp686B17277"
                                                                                                                                                                                                                                                                /gene="DKFZp686B17277"
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Enkaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 975)

S NIH-MGC http://mgc.nci.nih.gov/.

Interpolate (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Location/Qualifiers

Location/Qualifiers
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/clone_lib="NIH (phage-resistant)"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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BM460277
BM460277.1 GI:18509317
EST.
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                                                                                                  841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1197; Conservative 0; Mismatches
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                                                                                                                                                                                                     Location/Qualifiers
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/tissue_type="ductal carcinoma, cell line"
/lab host="mild" (phage-resistant)"
/clone_lib="NIH_MGC_ll0"
/clone_lib="NIH_MGC_ll0"
/clone_lib="NIH_MGC_ll0"
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/And sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capaba-ramail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga-llnl.gov
Plate: LLCM2390 row: o column: 22
High quality sequence stop: 535.
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  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.1%; Score 635; DB 5; Length 917; Best Local Similarity 100.0%; Pred. No. 0; Matches 635; Conservative 0; Mismatches 0; Indels
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230 Constitution Drive, Menlo Park, CA
721: 650 473 9658
Fax: 650 473 7760
Email: rbrandenbergerogeron.com
Insert Length: 753 Std Error: 0.00.
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Regenerative Medicine
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/cell_type="Lymphoblast-like"
/cell_type="Lymphoblast-like"
/cell_time="SNU-16"
/lab_host="DH10B"
/clone lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the Soraes laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
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K-EST0094733 S22SNU16n1 Homo sapiens CDNA clone S22SNU16n1-102-H01
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I (bases 1 to 622)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
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                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consider Account of the Constitute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Email: yongsung@mail.kribb.re.kr Plate: 102 row: H column: 01 High quality sequence stop: 622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.3%; Score 622; DB 3; Length 622; llarity 100.0%; Pred. No. 3e-308; Conservative 0; Mismatches 0; Indels
                                                                                                             644 AGCCTGCCCAGCACTTTGCCAGTAGTCCTCGTGG 678
                                                                                         601 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGG
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Unpublished (2002)
Contact: Kim YS
Genome Research Center
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-102-H01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'tissue_type="Ascites"
                                                                                                                                                                                                                                                                                                          BM823479.1 GI:19179892
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                        , mRNA sequence.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATG 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 TACGCGGCATCATTCGCATTAGTACCCGAAAAGACCGTGCTCGCCCACAGACCTCGGAGG 695
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1 (bases 1 to 582)

2 (bases 1 to 582)

Mizuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                        CTGATCGTGCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCA
                                                                                           Gaps
from DMSO-treated hES cell line H9 (p22) maintained feeder-free conditions"
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                           Length 753,
                                                                                        0; Indels
                                                           Score 598; DB 7; Le
Pred. No. 7.1e-296;
                                                         Query Match 34.9%; Score 598; DB Best Local Similarity 100.0%; Pred. No. 7.1 Matches 598; Conservative 0; Mismatches
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BP315176.1 GI:52244151
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AA316608 510 bp mRNA linear BST 19-APR-1997
BST188290 HCC cell line (matastasis to liver in mouse) II Homo
sapiens cDNA 5' end, mRNA sequence.
AA316608
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                            1. .582

| organism="Homo sapiens"

| organism="Homo sapiens"

| organism="Type="mana"

| db xere="exxon:9606"

| clone="OFR07979"

| clone="Sugano cDNA library, mammary gland OCUB-F"

| note="mammary gland tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 GACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCCAACCGCTGCTGCCCCCTGACAGTGG
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1 (bases 1 to 510)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
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                                                                                                                                                                                                                                                                                                                                                   Length 582
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                                                                                                                                                                                                                                                                                                                                                   30.8%; Score 528; DB 3; I
99.8%; Pred. No. 7.9e-260;
iive 0; Mismatches 1;
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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Homo sapiens (human)
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1181 bp DNA linear GSS 02-JUN-2005 gene, VIRTUAL TRANSCRIPT, partial
                                                                                      361 TTCCATGAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAA 420
                                                                                                                                                                                                                         715 ATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAG 774
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae, Pan.
1 (Dases 1 to 1181)
Nieleen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
Mite,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            820 AAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCT
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1181;
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Pred. No. 9.6e-241;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQ045549 1181 bp
Pan troglodytes FLJ34633 gene, VIR
sequence, genomic survey sequence.
DQ045549 GI:66896764
GSS.
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/gene="FLJ34633"
/locus_tag="HC11301"
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Best Local Similarity 99.8%;
Matches 541; Conservative (
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehn, C.L., Hamma, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.W., Relley, J.C., Liul, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Philips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.T., Pelligrino, S.M., Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, J.F., Li, Y., Benarik, D.P., Feng, D.F., Ferrie, A., Tsacher, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melsner, P.S., Olsen, H., Raymond, L., Wai, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nuclecides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 ACTGAGGGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCT 414
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byc clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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/cell_line="KM12C(HCC)metastasis into mouse (liver)"
/clone_lib="HCC cell line (matastasis to liver in mouse)
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Tel: 3018699056
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/db_xref="ATC" (inhost):113362"
/db_xref="taxon:9606"
/tissue_type="colon"
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The Institute for Genomic Research
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 81 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 432.
                                                                                                                                                                                                    GGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGCAGATCTCC 1059
                                                                                                                                                                                                                                        1000 GCCATGAGACCATGGTGGGCTCAGGTCTCAGGCAGGATGAGCTGACAGTGCAGATCTCC 1059
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                                                                 GAGGCCCCCTGGTACGCGCCATCATTCGCATTAGTACCCCGAAAGAGCCGTGCTCGCCCA 939
                                                                                                                      CAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGT 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="NCI CCAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: Sal1;
Note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-01!
AAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCT 879
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 489)

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
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                                          GAGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCA
                                                                                                                                                            940 cagaccrossassercerroaacrossecrecroscocaaccerrocccrosser
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2456810"
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Manufala; bulnelia; Educinoglines; Filmates; Catalinin; Hominidae; Homo.

1 (bases 1 to 470)

8 Bearl, L., Henli,O., Hennig,S., Neubert, P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B., Partsch,E., Peters,M., Human UnigeneSet - RZPD3

1 Unpublished (2003)

1 Unpublished (2003)

1 Contact: Ina Rolfs

1 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAG98803610.

1 RZPD: IMAG98803610.

1 RZPD: IMAG98803610.

1 RZPDILIB, I.M.A.G.E. cDNA Clone Collection;

1 RZPDILIB, I.M.A.G.E. cDNA CloneCards/Cgi-hin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

1 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany

1 Rel 49 30 32639 111

1 www.rzpd.de

1 RZPD (clone@rzpd.de) for further information. Seq primer: Contact RZPD (clone@rzpd.de) for further information. Seq primer: Location/Qualifiers
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470 bp mRNA linear EST 07-FEB-2003
BX110746 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGp998E036110 ;
IMAGE:2456810, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTCTGATCCCTGCCAGGCCCCTTCCTTCCTGCTCATGGTCTTCAGGTGGCCTGATCA 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1517 GCCACCCTAACCAATCATGCAAACTTCTCCCTGGGGGTAATTCAACAGTTAAAAGAA 1576
                                                                                                                                                                                                             430
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                     TGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCCTGCCTTGGCTGACTGG
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                                                                                                                                        1217 CCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGGGGACCAGGAACCCCTG
                                                                           Gapa
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          Length 489;
                                                                           0; Indels
28.0%; Score 480; DB 1; Le
ilarity 100.0%; Pred. No. 4.1e-235;
Conservative 0; Mismatches 0;
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/clone='IMAGE:196020"
/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/tab_hote="lub."
/lab_hote:"lub."
/lab."
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLML at: image.llnl.gov
Plate: LLCM842 row: g column: 05
High quality sequence stop: 668.
Location/Qualifiers
1. .966
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BP331524 Sugano cDNA library, rectum Homo sapiens cDNA clone
RCT09504, mRNA sequence.
Consortium (LLNL)
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100.0%; Pred. No. 1.2e-219;
tive 0; Mismatches 0;
cDNA Library Arrayed by: The I.M.A.G.E.
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                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity
Matches 450; Conservat
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                                                                 /mol_trpe="mana" creek
/db xref="taxon:606"
/clone="lwadp98E036110; IMAGE:2456810"
/tissue type="poorly differentiated adenocarcinoma with
/tissue type="poorly differentiated adenocarcinoma with
/lab_hogt="buld"
/lab_hogt="buld"
/clone lib="NuC CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: Sal1;
/site 2: Not1; Cloned unidirectionally. Primer: Ōligo dT.
/Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 966)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.3%; Score 450; DB 5; Length 470; 100.0%; Pred. No. 1.1e-219; ive 0; Mismatches 0; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                      organism="Homo sapiens"
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            Hominidae; Homo.

I (bases 1 to 583)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
Block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                   Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                        24.8%; Score 424; DB 3; Length 583; 100.0%; Pred. No. 2.9e-206; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              /tissue_type="rectum"
/clone_lib="Sugano cDNA library, rectum"
                                                                                                                                                                                                                                   1. .583
/organism="Homo sapiens"
                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RCT09504"
                                                                                                                                                                                                                   Location/Qualifiers
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Homo sapiens
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:

image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 361.
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13 bp mRNA linear EST 25-JUN-2003
EST19181 human nasopharynx Homo sapiens CDNA, mRNA sequence.
CD702656
CD702656.1 GI:32233286
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Hominidae, Homo.
I (bases 1 to 370)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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VERSION
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

Www-bio.llhi.gov/bbrp/image/image.html
Insert Length: 236 Std Error: 0.00
Seq primer: -40UP from Gibco.

Location/Qualifiers
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Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Best Local Similarity 100.0%; Pred. No. 3.1e-153;
Matches 321; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
                      Tumor Gene Index
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                   and
                                                                         Euteleostomi;
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/organism="Homo sapiens"
/organism="RNA"
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/tissue type="normal nasopharynx"
/clone_Tib="human nasopharynx"
/nore="ESTS generated from a normal nasopharynx cDNA
library from southern Chinese"
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                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostc
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
Liu, K.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G.
Zeng, Y.-X.
                                                                                                                                                                                                             Transcriptional Gene Expression Profile of Human Nasopharynx
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                                                                                                                                                                                                                                                                                                       Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
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1 (bases 1 to 330)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
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                          Homo sapiens (human)
                                                                                                                                                                                                                                     Unpublished (2003)
Contact: YiXin Zeng
Cancer Center
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Best Local Similarity 100.
Matches 323; Conservative
                                                Homo sapiens
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nk07d10.81 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1012819 3',
                                                                                                     AA573775.1 GI:2348290
                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
                                    mRNA sequence.
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/UDSILVENIE ... TOOMING SALVELUS
/UDSILVENIE ... TOOMING SALVELUS
/UDONE ... TAMAGE: 3947861"
/Lissue type="adenocarcinoma cell line"
/Lissue type="adenocarcinoma cell line"
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/Lissue type="adenocarcinoma cell line"
/Lissue type="adenocarcinoma cell line"
/Lissue Libe Nor Lipe your portal site 1: XhoI; Site 2:
/Loue libe Nor Nor Lipe Nor Lipe Salve Salve following 5:
adaptor: GGCACGAG(G). Size-selected >SoUbp for average
lisert size 1: 8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM810 row: d column: 06
High quality sequence stop: 752.
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                                                                                          Hominidae, Homo.

1 (bases 1 to 1015)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 99.5
Matches 403; Conservative
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ORGANISM
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AUTHORS
TITLE
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CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrpt/image.html
Insert Length: 635 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 465.

1. .556

1. .556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 creciriocarececaderigarerecisecadodececerrecirios de 257
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                        Hominidae; Homo.

1 (bases 1 to 556)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496 CTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGG
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                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
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                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
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Best Local Similarity 99.6%; Pred. No. 9.1e-138;
Matches 461; Conservative 0; Mismatches 1;
                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1012819"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., Ph.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., Ph.D., CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1538 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
                                                                                                                                                                                                                                                                                              AW008047 1NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2532827 3',
                       1618 ACTCTATGTTATGTTAAGGAGTTGGTTCTTGGTTCTTGGCTGATGTTCTGTATCTTAACAT 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1311 TGGCTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGG 1370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: scomach; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 ACTCTATGTTATGTTAAGGAGTTGGTTCTTGGTTCTTGGCTGATGTTCTGTATCTTAACAT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Gas4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                      AW008047.1 GI:5856825
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
AW008047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Matches 385; Conserv
                                                                                                                       1678 GACC 1681
                                                                                                                                                                         34 GACC 31
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AW008047/c
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CAPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llni.gov/bbrp/fimage/fimage.html
Seq primer: -40UP from Gibco
High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="carcinoid"
/lab host="DH10B"
/clone_lib="NCI_cdpe_Lub"
/clone_lib="NCI_cdpe_Lub"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from meroendoorine lung; vector: ps. strand cDNA was prepared from not Eco RI adaptors (Pharmacia), digested with Not I and to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pl7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                 AI216202 412 bp mRNA linear EST 22-OCT-1998
qm; e07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1884036 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1438 TCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACC 1497
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.

1 (bases 1 to 412)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                  1560 TICAACAGITAAAAGAAGCITAICITAAAIGIAITGIATIGGG 1602
                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE:1884036"
                                                                                                                                                                                                                                                                                                                                                                            AI216202.1 GI:3785243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .412
                                                                                                                                                                                                                                                                                                                               nRNA sequence.
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Matches 244; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                       RESULT 19
AI216202/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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Contact: Kim YS
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JOURNAL
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BM750392
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BE162756.
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1 (bases 1 to 244)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deoliveira,P.E., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
CAGGCCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PMI-HT0454-170 Seq primer: puc 18 forward
                                                                              CAGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT 34
                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                               CCTGGGGTAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATTGGGGGGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.4%; Score 213; DB 2; Length 244; 100.0%; Pred. No. 1.2e-97; tive 0; Mismatches 0; Indels
                                                                                                                                                                                      CTTAACATGACCACAGTTTGTAAGTAC 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 244. Location/Qualifiers
                                                                                                                                                                                                      CTTAACATGACCACAGTTTGTAAGTAC 7
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                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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AUTHORS
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BE162756
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Gaps ö

Best Local Similarity 100. Matches 213; Conservative

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/tissue type="Stomach"
/cell_type="Epithelial"
/cell_type="Epithelial"
/cell_type="Epithelial"
/cell_type="Epithelial"
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/cell_type="Epithelial"
/lab host="ToploF"
/loce="Organ: Stomach; Vector: pCNS; Site_l: EcoRI;
/note="Organ: Stomach; Vector: pCNS; Site_l: EcoRI;
/site_2: Not!; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (RAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intect mRNA was ligated with backer with drawa such and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 6ont. The CDNA vector was circularized with B. coll DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Odsayama elect method. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM750392 246 bp mRNA linear EST 04-MAR-2002
K-EST0025949 S7SNU719 Homo sapiens cDNA clone S7SNU719-1-G12 5',
mRNA sequence.
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1 (bases 1 to 246)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                     446
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                                                                                                                                      CAGCCCTGCCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 148
                                                                                                                                                                                                                                                                                327 CAGCCCCTGCCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 386
                         88
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
CTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAGCCTGTGTGCGGGGATG
                                                                                                                                                                                                                                     GGAGCACAATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCCCAGCCGGCGGGATGGCCA
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Eax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: G column: 12
High quality sequence stop: 246.
                                                                                                                                                                                                                                                                                                                                                                           447 GCGGCTCAAGTCAACCATGGGCAGCAGCTTCAG 479
                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCTCAAGTCAACCATGGGCAGCAGCTTCAG 241
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Unpublished (2002)
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="S7SNU719-1-G12"
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/clone='IMAGE:3629484"
/tissue type="choriocarcinoma"
/tissue type="choriocarcinoma"
/tab_hofe="blue"
/lab_hofe="blue"
/lab_h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE409561 11H_MGC_21 Homo sapiens cDNA clone IMAGE:3629848 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GCTTATCTTAAATGTATTGTATTGGGGGGTGGGCAGGCCCCACTCTATGTTATGTTAAGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDN Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM317 row: a column: 17
High quality sequence start: 19
High quality sequence stop: 482.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              60 GCCACCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTCAACAGTTAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1577 GCTTATCTTAAATGTATTGTATTGGGGGGGGGGGGGGGCCCACTCTATGTTAAGG
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1 (bases 1 to 1092)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                           Length 291;
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                                                                                                                                                                       10.5%; Score 180; DB 2; L 100.0%; Pred. No. 1.3e-80; ive 0; Mismatches 0;
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.00.0%; Pred. No. 3.3e-68;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE409561.1 GI:9346011
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BE409561
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BE409561
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/otone_lorgan: head neck; Vector: puc18; Site_1: Smal;
/note="Organ: head neck; Vector was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
% 196,716 - Ludwig Institute for Cancer Research)
                                                                                                                                                                                                                                                    1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunsteain, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                           1549 CCCTGGGGTAATTCAACAGTTAAAAGGCTTATCTTAAATGTATTGTATTGGGGGGGTGG 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1609 GCAGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTA 1668
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-HT1265-170401-002-d07&t3=2001-04-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence start: 284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG998476 291 bp mRNA linear EST 13-JUN-2001
MR4-HT1265-170401-002-d07 HT1265 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 GCAGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTTGTA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                    1489 GAGTGAACCCTGACTCCATCCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCT
                                                                                                                                                                                                                                                                                                                     28 GAGTGAACCCTGATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCT
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                                                                                                         Length 246;
                                                                                                                                                                               Indels
   full-length enriched cDNA library."
                                                                                                         12.1%; Score 208; DB 3; I
100.0%; Pred. No. 4.7e-95;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1669 TCTTAACATGACCACAGTTTGTAAGTAC 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 TCTTAACATGACCACAGTTTGTAAGTAC 235
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                                                                                                                                                 Best Local Similarity 100.
Matches 208; Conservative
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                                                                                                                                              Similarity
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COMMENT
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BG998476
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                                           DRIGIN
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/tissue_type="foriocarcinoma"
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/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Diectionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGGACGAG(6). Size-selected >SOObp
for average insert size 1.8kb. Library constructed by
infig Hong in the laboratory of Gerald M. Kubin (University
of Galifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              # 450 bp mRNA linear EST 16-JAN-2001 RC0-FN0204-221200-022-b01 FN0204 Homo Bapiens cDNA, mRNA sequence.
BF856421.1 GI:12244165
                                                                                                               AW732798 139 bp mRNA linear EST 21-APR-2000
bb14f07.yl NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2962885 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

Seq primer: -40RP from Gibco

High quality sequence stop: 112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 CTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCAGCCGGCG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 GGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGGATGTTAAGCT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCATCAGCTACCCCCGATGTTAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCG 60
                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                 NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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205 IGCCGGGCTGCCTTCTGCTTCCGCC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 CAAAGGCATCCCTGTGTAT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAGGCATCCCTGTGTAT 139
                                                                                                                                                                                                            AW732798.1 GI:7633136
                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                     EST.
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AW732798
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                                                                                                                                                                                                                                                                                                                                                    BE741110 623 bp mRNA linear EST 15-SEP-2000 601593919F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947885 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="addinger-resistant)"
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                                                                                                                 218 AAGCCGCCGCACCCGTAGACCACGACCCCAAGGACCCTGGCCATGGGCCCAGAGAGCAT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 6 GACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTCATCTCTGGCTCTGCT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACCCCAAGGACCCTGGCCACCATGGGCCAGAGGAGCATTACCTTCATCTCTGGCT 144
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                                            GTGGGAGCGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                           AAGCCGCCGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCCAGAGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.

1 (bases 1 to 623)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
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100.0%; Pred. No. 1.4e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/clone="IMAGE:3947885"
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BE741110
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                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (bases 1 to 277)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GGCCTCCACGCTTGGGACCGTGGGAGCGGCCAACAGAGCTATGTCTGGAGACATATGATA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 bp mRNA linear EST 23-SEP-2
DKFZp469G0138 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469G0138 5', mRNA sequence.
CR76381s
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
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                                                                                                                                                                                                                                                                        Kim, Y.S.
21C Frontier Korean EST Project 2001
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/db_xref="taxon:9606"
/clone="S9SNU601-20-C05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: yongsung@mail.kribb.re.kr
Plate: 20 row: C column: 05
High quality sequence stop: 277.
Location/Qualifiers
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CR763815.1 GI:52602277
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sapiens (human)
                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: Kim YS
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Best Local Similarity 100.0
Matches 101; Conservative
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                                       Homo sapiens
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                                                                                                                                                                    Hominidae; Homo.

1 (Dases 1 to 450)
Diasa Neto, E., Garcia, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ081980 277 bp mRNA linear EST 04-APR-2002 K-EST0026481 S9SNU601 Homo sapiens cDNA clone S9SNU601-20-C05 5', mRNA sequence.
BQ081980 GI:19938986
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpsonolluwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-FN0204-221200-022-b01&t3=2000-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 446.
High quality sequence stop: 446.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: prostate_normal; Vector: puc18; Site_1: Snal; Site_2: Snal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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316 CTTCTCCCTCCCTGGGGTAATTCAACAGTTAAAAGAAGGT 355
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0204"
                                       sapiens (human)
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Fax: +55-11-2707001
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This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKF2);
Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG315647 101H_MGC_21 Homo gapiens cDNA clone IMAGE:4541898 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GAGCGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="469 (synonym: pkid1)"
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                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                   Hominidae, Pongo.

1 (bases 1 to 276)
Ansorge, W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                Pongo pygmaeus mRNA (Ansorge,W., Krieger,S., Regiert,T., et al.)
Unpublished (2004)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
dammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="DKFZp469G0138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG071655
Par troglodytes DNA, clone: PTB-062016.F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAAC 97
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7.9e-38;
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100.0%; Pred. No. ...
... 0; Mismatches
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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http://image.llnl.gov
Plate: LLCM1221 row: c column: 19
High quality sequence stop: 496.
Location/Qualifiers
                                                                                                                                                                                          1. .928
/organism="Homo sapiens"
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AG071655.1 GI:16623457
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Best Local Similarity 100..
Best Acceptance
The P7; Conservative
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                                                                                                                               DEFINITION
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Matches
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AUTHORS
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JOURNAL
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                                                                                                                                                                       ACCESSION
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KEYWORDS
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KEYWORDS
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                                                                                             BG335025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                                                                                             1244 CTACAGAATGAAGAGGGGACCAGGAACCCCTGTGGGAGGCCTTAGACCTGAAGCAGTG 1303
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                    Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Obackenbush, J. and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
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/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                           Gaps
                                                                                                                                                                                           ..
0
                                                       /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                   5.0%; Score 86; DB 10; Length 677;
100.0%; Pred. No. 3.6e-32;
ive 0; Mismatches 0; Indels
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3.4%; Score 59; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 59; Conservative 0; Mismatches 0; Indels
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239074 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF191474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
USDM, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                        1304 CCCACTCTGGCTCCTCCTGCCTTGGC 1329
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-062016.F"
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
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Plate: 66 row: F column: 19
Seg primer: ATTTAGGTGACATARG.
Location/Qualifiers
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                         86; Conservative
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Sus scrofa
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COMMENT
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BF191474
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Gaps

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790 TCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCAC 848

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/tissue type="choriocarcinoma"
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/clone lib="NIH MGC 21"
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602403470F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541320 5',
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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E. 1 (bases 1 to 1088)
S. NIH-Mac http://mac.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://imagge.llhi.gov
Plate: LLCM1219 row: & column: 17
High quality sequence stop: 556.
266 TCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 CACCATGAGCCAGAGAGCATTACCTTCATCTCTGGCTCTGAGCCGGCCCTTGAGT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 CACCATGGGCCAGAGAGCATTACCTTCATCTCGGCTCTGCCTGAGCCGGCCCTTGAGT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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/mol type="mRNA"
/db xref="taxon:9606"
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BG335025.1 GI:13141463
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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879 ATCAGCACCATCACGCAGGACTACCACCTGGATGAGCAG 917
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tes 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                      Porcine gene discovery by normalized cDNA-library sequencing and BST cluster assembly Mamm. Genome 13 (8), 475-478 (2002)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J., Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /_clone_lib="MARC_2PIG"
/note="Vector: pCMV SPORT6; Site_l: Not1; Site_2: Sal
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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100.0%; Pred. No. 5e-09;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR PRIMERS
FORWARD: AGGAAGCAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 30 row: H column: 14
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                              Contact: Smith TPL
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AUTHORS
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                                                                                  TITLE
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to prepare Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Wanardo, R., Wilming, L.G., Whynshaw-Boris, A., Yanagisawa, M., Yang, L., Yana, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Xaunishi, A., Yashino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length, CDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fel: 81-45-503-9212
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hort,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
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/clone_lib="RIKEN full-length enriched, 10 day old male
pancreas"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
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EST

DEFINITION

BX518790 LOCUS

ACCESSION

VERSION KEYWORDS

SOURCE ORGANISM

TITLE JOURNAL COMMENT

AUTHORS

REFERENCE

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EST 09-MAR-1998
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                            1 (bases 1 to 406)
Marram, "Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
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                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse BST Project
WashU-HHMI Mouse BST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA856355 491 bp mRNA linear EST
vw99g12.r1 Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1263142 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="13.5-14.5dpc_total_fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8; Le
1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.2%; Score 38; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: mob.REGA+ET
High quality sequence stop: 358.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:372517"
                         Mus musculus (house mouse)
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AA856355.1 GI:2944657
                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .406
                                                  Mus musculus
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KEYWORDS
SOURCE
ORGANISM
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                                                ORGANISM
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JOURNAL
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                                                                                                                                                                        AUTHORS
                                                                                                                                                 REFERENCE
KEYWORDS
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                    SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W61708 406 bp mRNA linear EST 07-JUN-1996 md57£07.rI Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:372517 5', mRNA sequence.
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                         EST 27-JUN-2003
                                                                                                                                                                                                                                                                                                                    Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free from RZPD; conteat RZPD; conteat RZPD (cloneerzpd.de) for further information. Seg primer: T7, Primer sequence: TAATAGGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                     Mouse UnigeneSet - RZPD2
Unpublished (2003)
Conteact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAG9991233179.
RZPD: IMAG9991233179.
RZPD: IMAG9991233179
RZPD: IMAG9991233179
RZPD: IMAG9991233179
RZPD: IMAG99981233179
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.plp.gaj/response7libNo-981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                    BX518790 area thymua 2NbMT Mus musculus cDNA clone IMAGP998L233179 ; IMAGE:1263142, mRNA sequence.
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100.0%; Pred. No. 1.8e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGp998L233179 ; IMAGE:1263142"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                       BX518790.1 GI:32300318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W61708
W61708.1 GI:1368457
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Best Local Similarity
                                                                                                   BX518790
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source

FEATURES

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DEFINITION

RESULT 37 W61708

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Matches

ORIGIN

ACCESSION VERSION

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This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@lange.lln.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 501)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidea; Muridae; Murinae; Mus.
           Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TT: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
/dev_atage="13.5-14.5dpc total fetus"
/dab_host="billob"
/clone_lib="Soares mouse embryo NbME13.5_14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZOS9937
RPCI-23-429E10.TV RPCI-23 Mus musculus genomic clone
RPCI-23-429E10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 500;
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 55
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Local Similarity 100.0%; Pred. No. 1.8e-07;
es 38; Conservative 0; Mismatches 0;
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                     1. .500
/organism="Mus musculus"
                                                                                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                    quality sequence stop: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:372517"
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                                                                                                                                                                                                                                                                                              Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus
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AZ059937.1 GI:7351186
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Unpublished (1999)
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POLYA=No.
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Matches
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    JOURNAL
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                       COMMENT
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Ten, F., Underwood, K., Morris, M., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R.
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1 (bases 1 to 500)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Ritter, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterstcon, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:665694
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                                                                                                                                          The WashU-HMM Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMM Mouse EST Project
WashU-HMM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Faz: 314 286 1810
Email: mouseest@watson.wustl.edu
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.2%; Score 38; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1263142"
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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source

FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS ö

ö

GSS 30-MAR-2000

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

LOCUS DEFINITION

AI425628

ORIGIN

ACCESSION VERSION

KEYWORDS

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/db_xref="taxon:10090"
/db_xref="taxon:10090"
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/lab_host="1010B (Life Technologies)"
/lab_host="1010B (Life Technologies)"
/clone lib="NHH BMAP MPG"
/note="Vector: pr773D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; The
NHH BMAP MPG library is a non-normalized library
constructed from mouse pineal gland. The tag is a string
of 5 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
79-806, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gex="maje and female"
/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
organ of Corti (OC) was fine dissected from a total of 386
cas follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 bp mRNA linear EST 19-JUN-2002 gi52a07.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi52a07 5', mRNA sequence.
BQ556109
BQ566109.1 GI:21469426
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing Unpublished (2002)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
(bases 1 to 535)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2%; Score 38; DB 2; Length 519;
100.0%; Pred. No. 1.8e-07;
tive 0; Mismatches 0; Indels
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Plate: 52 row: a column: 07
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                                                        organism="Mus musculus"
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/clone="gi52a07"
                                Location/Qualifiers
                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus
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Structural Cell Biology
        Seq primer: M13 Reverse
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Best Local Similarity 100.C
Matches 38; Conservative

    (bases 
Kachar, B.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (RRL Life Technologies). "
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UI-M-AO0-aca-d-03-0-UI.rl NIH BMAP_MPG Mus musculus cDNA clone
UI_M-AO0-aca-d-03-0-UI 5', mRNA sequence.
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EMAILE MEST@mail.nih.gov

CHOM Library Preparation: M.B. Soares Lab Clone distribution:

Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
                                                                                     Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
ABCPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgae.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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Mational Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-8643, USA
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9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200
Fax: 301 838 0208
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100.0%; Pred. No. 1.8e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="RPCI-23-429E10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Fax: 301 443 9890
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Matches 38; Conserva
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SOURCE
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DEFINITION
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AUTHORS
TITLE
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Gaps

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cervical dislocation followed by decapitation, the bullar was removed and opened in Leibowitz medium. The bony cappaule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1592-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Ptu DNA polymerase, ijated with EcoN was blunt ended with Ptu DNA polymerase, ijated with EcoN in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Seps00 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the thi-ZAP XR vector, which had been predigested with EcoN I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xil Blue MRF. "Cello I and the phage library was estimated to be 11,100,000 recombinants Stratagene's Exasist Interference resistence helper phage (catalogue # 211203) was adopted resistence belaemed DNA from the phages. Upon plating of the cecue plasmid DNA from the phages. Upon plating of the cecue plasmid DNA from the phages. Upon plating of the conting from 20 out of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen) which and of the conversion of the concert96 (TM) plasmid p
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BB657667 BIKEN full-length enriched, 12 days embryo eyeball Mus musculus cDNA clone D230011M17 5', mRNA sequence.
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                                                                   Query Match
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                                                                                                                                                      H3081C02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3081C02 5', mRNA sequence.
BG082830 GI:40069253
EST.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 2.2%; Score 38; DB 5; Length 535; 100.0%; Pred. No. 1.8e-07; iive 0; Mismatches 0; Indels
                                                                                      340 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 377
                                                                     835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
Query Match
Best Local Similarity 100.0
Matches 38; Conservative
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KEYWORDS
SOURCE
ORGANISM
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/lan_nose="Number 15K cDNA Clone Set"
/clone 115="NLA Mouse 15K cDNA Clone Set"
/note="Vector: pSPORT1; Site 1: Sall; Site 2: Not1; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7:5 embryos, extraembryonic part of E7:5 embryos.

All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse development cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3081 row: C column: 02
Seq primer: -21M13 Reverse
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
Sciurognathi; Muroidea; Murinae; Mus.
I (basea 1 to 586)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                        Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                              On Jan 26, 2001 this sequence version replaced gi:12565398.
Other_ESTs: H3081C02-3
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1.9e-07;
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 586
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                                                                                                                                                                                                                                                                                                            10922068
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Biract Submission

L Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokoham, Kanagawa, 230-0045, Japan

(B-mail: hattorieger.riken.jp, URL: http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

library availability, please contect Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                                                                                                                                                                                                                                                                                                                                 AG603040 763 bp DNA linear GSS 23-DEC-2004
Mus musculus molossinus DNA, clone:MSMg01-535K05.T7, genomic survey
was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
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tissue_type="mixture of kidney and spleen" /
clone_lib="MSMg01 Mouse Male BAC Library"
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1.9e-07;
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100.0%; Pred. No. 1.9
tive 0; Mismatches
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100.0%; Pred. No. 1.9
ative 0; Mismatches
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/sub_species="molossinus"
/db_xref="taxon:57486"
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Marches 38; Conservative
                                                                                                            Query Match 2.23
Best Local Similarity 100.
Matches 38; Conservative
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Konno, H., Fukunlahi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Pukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse CDNAs Compared with
                                                                                                                                                               1 (bases 1 to 601)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Umpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resease.riken.jp, URL:http://genome.gec.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/dev_stage="12 days_embryo"
/lab_host="DH108"
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                            Mus musculus (house mouse)
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JOURNAL
COMMENT
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     CEYWORDS
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/mol_type="mRNA"
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KEYWORDS
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 826)
S NIH-MGC http://mgc.nci.nih.gov/.
L National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM11955 row: 1 column: 09
High quality sequence stop: 796.
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918 bp mRNA linear EST 24-OCT-2000 e0177134F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014680 5',
                                                                                                                             BI694617
603347838F1 NCI_CGAP_Mam2 Mus musculus CDNA clone IMAGE:5375384 5',
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/note="Organ: mammary; Vector: pCWV-SPORT6; Site_1: SalI;
Salisale_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus Subrayos, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus. 1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
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462 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 425
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/clone="IMMGE:5375384"
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/lab_host="DH108"
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100.0%; Pred. No. 1.9e-07;
tive 0; Mismatches 0;
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/strain="FVB/N-3"
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AUTHORS
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KEYWORDS
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9259 row: d column: 09
High quality sequence stop: 653.
                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayd by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: Li_AMI1364 row: k column: 03
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602991514F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5147642 5',
mENA sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          835 ATCAGCACCACCAGGACTACCACCTGGATGAGCA 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%; Score 38; DB 2; Le 100.0%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0%; Pred. No. 1.9
Matches 38; Conservative 0; Mismatches
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High quality sequence stop: 840.
Location/Qualifiers
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Mus musculus
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100.0%; Pred. No. 2e-07;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                          full insert sequence.
AK051860
AK051860.1 GI:26342255
                  38; Conservative
                                                                                                                                                                                                                                                                            HTC; CAP trapper.
                                                                                                                                                                                                                                                                                                                 Mus musculus
 Local Similarity
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SOURCE
ORGANISM
                                                                                                                                     RESULT 50
AK051860/c
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VERSION
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PUBMED
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JOURNAL
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NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
          /clone lib="NCI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sal1; transgenic model WNT-1, expression driven by AMTV-LIR enhancer; Cloned unidirectionally. Primer: Oligo MT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF135747 984 bp mRNA linear BST 24-OCT-2000 601781110F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008914 5',
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                 Gaps
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                 Length 930;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    121 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 158
                                                                                                                                                                                                                                                                                                                                                                                   835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
                                                                                                                                                                                                                                                                                                               Score 38; DB 3; L
Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                              / Match
Local Similarity 100.0%; Pred. No. 1.9
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High quality sequence stop: 629.
Location/Qualifiers
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/clone="IMAGE:4008914"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Czech II"
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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2.2%; Score 38; DB 2; Length 984;

Query Match

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AKO51860 1596 bp mRNA linear HTC 03-APR-2004 Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230011M17 product:hypothetical protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1556)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
    Gaps
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Indels
                                                                                          835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
                                                                                                                                              237 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 274
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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JOURNAL
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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Harah, A., Hayateu, N., Hiramoto, K., Hiramoto, K., Hiramoto, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Shinatak, T., Sogabe, Y., Shinatak, K., Shinatak, T., Sogabe, Y., Suzuki, H., Toya, T., Yamamura, T., Yashashi, F., Tanaka, T., Yoshino, M., Muranatsu, M. and Hayashizaki, Y., Tohida, K., Sohino, M., Muranatsu, M. and Hayashizaki, Y. Direct Submission Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Exploration Research Group, RIKEN Genomic Sciences Center (SGC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseggscriken.jp, Vokohama, Please visit our web site (http://genome.gsc.riken.jp/) for further derails
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter of sequence[5].
   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saaaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_grage="10 day old"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/strain="C57BL/6J"
/db_xref="RANDM DB:1810019J16"
/db_xref="taxon:10090"
/clone="1810019J16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_steage="12 days embryo"
890. .1432
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GLQPRTQAPQRCRQSLQRRKQXAALHQSQPQGRQRRQQVGGSLAGSAEPEMKVILSGP
WWPGSLGSGLLVRRPGGGWERSSFVSRHNSDGLSQGPKRGGPDDGRGCPGLGMAQSMA
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                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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(evidence: decoder,Longest-ORF)
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Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Managawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
1..1596
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:D230011M17"
/db_xref="taxon:10090"
/clone="D230011M17"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/protein_id="BAC34790.1"
/db_xref="G1:26342256"
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Department of Molecular. Cell Pharmacology
National Research Institute for Child Health and Development
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Tel: 81-3-3149-1252
Email: 91-3-3149-1252
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This work was performed to collaborate with Developmental Biology
This work was performed to Collaborate with Developmental Biology
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8833 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System
(ORCS) project of Ministry of Education, Culture, Sports, Science
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
Suzuki, Y., Tsujimoto, G., Izaike, Y., Todoroki, J. and Hashizume, K.
Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray
Mol. Reprod. Dev. 65 (1), 9-18 (2003)
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Subtraction by Bento Soares and M. Fatima Bonaldo.
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/dev_stage="adult"
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                                                                                                                                          Query Match 2.2%; Score 37; DB 1; Length 488; Best Local Similarity 100.0%; Pred. No. 5.9e-07; Matches 37; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.5e-06;
ive 0; Mismatches 0;
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/db_xref="taxon:9913"
/clone="ORCS11684"
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1 (bases 1 to 605)
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Location/Qualifiers
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Contact: Gozoh Tsujimoto
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                                                                              DRIGIN
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/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capable-remail.n.ih.gov
Contact: M.D., Ph.D.
Contact: M.D., Ph.D.
Contact: Preparation: M. Bento Soares, Ph.D.
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GVPPSPDRAPFSRRDGQRLXTSMGSSFSYPDYKLKGTPVYPYRHATSPVPDVDSCCKB
BLABPPPTRHSLDSTFTNSPRGSEFSYPSPNSTDLDFBRGSGSNSSREIDVLIFKKLT
BLESPPTRHQIDELAKCTSPTPVFLEKTSKISDLISSITQDYHLDEQDAEGRLVRGIIRIST
RKSRSRPQTSERRSARGYPAPAAPDSGHETMLGSGLSQDBLIYQISQEFTAADAIRKL
RPYGAPGYPASQDSSFQGTDTDSSGAPLLQVYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI669760 488 bp mRNA linear EST 15-DEC-1999 1112h08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2250879 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                          translation="mSAPSPHRAVAPGGQTLRTLATTGQRVSPSFQALQNQPTSPQPA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 488)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, C1, 130KD homolog [Mus musculus] (SPTR|Q922Q0, evidence: FASTY, 97.2%ID, 100%length, match=649)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%; Score 38; DB 4; Length 1657; llarity 100.0%; Pred. No. 2.1e-07; Conservative 0; Mismatches 0; Indels
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 792 Std Error: 0.00
Seq Primer: -400P from Gibco
High quality sequence stop: 452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
                                                                                                                                                                                /proteIn_id="BAC25177.1"
/db_xref="GI:26357449"
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/db_xref="taxon:9606"
/clone="IMAGE:2250879"
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/lab_host="DH108"
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                                                                                                            putative"
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AI669760
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A1669760/c
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TITLE
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Gaps

us-09-989-890-105.oligo.rst

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CB759331 434 bp mRNA linear EST 16-MAY-2003 AMGNNUC:NRPI4-00055-F9-A W Rat pituitary (10472) Rattus norvegicus CDNA clone nrpi4-00055-F9 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE533148 609 bp mRNA linear EST 09-AUG-2000 601235445F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3599314 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/clone="mpi4-00055-£9"
/clone=lib="W Rat pituitary (10472)"
/note="Vector: pSPORTI; Site I: Sall; Site 2: Not1; W Rat pituitary adult female Wistar rat avg insert size 2: kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                              /cell type="Embryonic Stem Cell"
/clone lib="Sanger Institute Gene Trap Library pGT2lxr"
/note="Vector: pGT2lxr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881
Plate: 00055 row: f column: 9.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                1.7%; Score 29; DB 10; Length 260; 100.0%; Pred. No. 0.0074; Live 0; Mismatches 0; Indels
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5. 0.0078; 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .434
/organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                       208 TTCAAGAAGCTGAAGAGCTGTTCAGCGT 180
                                                                                                                                                                                                                                                                                                                                                                                  730 TTCAAGAAGCTGACAGAGCTGTTCAGCGT 758
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                                                   organism="Mus musculus"
                                                                    /mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
Rattus norvegicus
       Location/Qualifiers
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dan Fitzpatrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 434)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
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EST.
                                                                                                                                                                                                                                                                                                                                 29; Conservative
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BE533148
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Matches 29; Conserv
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KEYWORDS
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CB759331
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
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BE533148
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KEYWORDS
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murcidea; Muridae; Mus.

B 1 (bases 1 to 260)

S anger Intitute Gene Trap Resource - SIGTR.

http://www.sanger.ac.uk/PostGenomics/genetrap/

Unpublished (2003)

On Feb 25, 2005 this sequence version replaced gi:60285534.

Contact: Sanger Institute Gene Trap Resource - SIGTR

Wellcome Trust Sanger Institute

Email: info.genetrapgeanger.ac.uk

Sequence tag generated by 5, RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from Sanger Institute Gene Trap

Resource. Annotation information available from

http://www.sanger.ac.uk/PostGenomics/genetrap/

Class: Gene Trap.
                                                                                                                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: LAM8004 row: M column: 8
Seq primer: GTAATACGACTATAGGG.
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Peccara; Bovidae; Bovinae; Bos.

1 (bases 1 to 585)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Contact; Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CW991025 260 bp mRNA linear GSS 20-JUL-2005
BC0173 Sanger Institute Gene Trap Library pGT21xr Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="WARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: BcoR1; Site 2: Not1;
Library made with RNA pooled From multiple tIssues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
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                                                Bos taurus (cow)
    CB463434.1
                                                                    Bos taurus
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Musualia; Butheria; Buarchontoglires; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 756)

1 (bases 1 to 756)

1 (bases 1 to 756)

1 (bases 1 to 756)

2 (Contact: Rober Strausberg, Ph.D.

2 Contact: Rober Strausberg, Ph.D.

2 Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llll.gov

Plate: LLAM10845 row: c column: 22

High quality sequence start: 114

High quality sequence stop: 750.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG871324 1NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923597 5',
                                                                                                                /db xref="taxon:10090"
/clone="IMAGE:5005226"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH108"
/lab_host="OH108"
/note="Organ: mammary; vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: NOTI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_SG2"
                                                                                                                                                                                                                                                                                                                                                                                                              1.7%; Scor.
100.0%; Pred. No. v...
0; Mismatches
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100.0%; Pred. No. 0.0
iive 0; Mismatches
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                 organism="Mus musculus"
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                                                                                         strain="FVB/N-3"
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BG871324.1 GI:14221864
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Matches 29, Conservative
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Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gex="female, virgin"
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1; Site_2: NCI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabe=remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LiAMB781 row: i column: 11
High quality sequence stop: 587.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Techhologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.m.column: 03
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                    1 (bases 1 to 609)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                    Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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BI078885.1 GI:14497215
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Matches 29; Conservative
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AL730744 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA clone BNOAA116ZH12 5', mRNA sequence.
                                                                                                                                                                           Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

(Colmbra, R. Weil, D., Brottier, P., Blanchard, S., Levi, M.,
A subtracted CyNA library from the zebrafish (Danio rerio)

embryonic inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi; Actinopterygii, Neopeerygii, Teleostel; Ostariophysi; Cyprinidae; Danio.

1 (bases 1 to 629)

2 (colmbra, X., Well, D., Brottier, P., Blanchard, S., Levi, M., Hardellin, J. P., Weissenbach, J. and Perit, C.

A gubtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
AL724130 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BN0AA0732B04 5', mRNA sequence.
AL724130
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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100.0%; Pred. No. 0.026;
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live 0; Mismatches
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/organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                       AL724130.1 GI:20188734
                                                                                                                                                      Danio rerio (zebrafish)
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Unpublished (2002)
Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
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AL730744/c
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                                                                                   ACCESSION
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KEYWORDS
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Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
tto H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                            BF041373 485 bp mRNA linear EST 10-OCT-2000 BP250025B20B12 Soares normalized bovine placenta Bos taurus cDNA clone BP250025B20B12 5', mRNA sequence.
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/clone_lib="Soares normalized bovine placenta"
/clone=Torgan: placenta; Vector: pT713Pac; Site 1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; pecora; Bovidae; Bos.
1 (bases 1 to 485)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Lewin, H. A.
W. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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BACKWARD: ATTAACCCTCACTAAAG
INSert Length: 485 Std Error: 0.00
Plate: BP250025B20 row: B column: 12
Seg primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 485.
                                                                                216 AAGGACCCTGGCCACCATGGGCCAGAGAG 244
                                                      142 AAGGACCCTGGCCACCATGGGCCAGAGAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 CCTGCTGCTGCTCTGGCGACCCTGGGT 245
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/clone="BP250025B20B12"
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                                                                                                                                                                                                                                                                                                                             BF041373.1 GI:10758428
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Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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source

FEATURES

7.4

RESULT 61 AL724130/c LOCUS

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Matches

ORIGIN

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Gaps

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Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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I (bases 1 to 535)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40UP from Gibco
High quality sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="wpils.pk007.a7"
/tissue_type="leaf"
/tissue_type="leaf"
/clone_lib="wpils"
/note="Vector: PGEM-T Easy; Site_1: Smal; Wheat, Polk
cultivar (resistant), infected with septoria tritici
strain A 24 hours after infection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI267255 aq62h05.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE22035545, mRNA sequence.
                                                                                                                                                        Crop Genetics
E. I. DuPont de Nemours and Company
I Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2602
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/organism="Homo sapiens"
/dol_type="mRNA"
/clone="IMAGE:2035545"
/clssue type="frontal lobe (see description)"
/lab_hogt="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 27; DB 6; Length 369;
100.0%; Pred. No. 0.082;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
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AI267255.1 GI:3886422
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AI267255/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

( bases I to 765)

Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue type="inner ear"
/dev_stage="embryonic"
/clone_lib="banio rerio embryonic inner ear subtracted
      /clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner ear subtracted cDNA Danio
                                                                                                                                                                                                                                 Gaps
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Location/Qualifiers
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100.0%; Pred. No. 0.027;
tive 0; Mismatches 0; Indels
                                                                                                                                                                  Length 629
                                                                                                                                                           Query Match 1.6%; Score 28; DB 1; Length 629
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 28; Conservative 0; Mismatches 0; Indels
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AL715958 Danio rerio embryonic inner ear subtracracric CDNA clone BN0AA0112E08 3', mRNA sequence. AL715958
                                                              /note="subtracted cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="subtracted cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BNOAA011ZE08"
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                 31 TIGTAAGTACCTCGGCCGCGACCACGC
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Unpublished (2002)
Contact: Genoscope
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Best Local Similarity
Matches 28; Conserva
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CA736276
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Gaps

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EST 17-NOV-1998

Length 600;

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Query Match 1.6%; Score 27; DB 6; Best Local Similarity 100.0%; Pred. No. 0.086; Matches 27; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                              AL718806.1 GI:20183410
                                                                                                                                                                                                                                                                                                                                                  Danio rerio (zebrafish)
Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      embryonic inner ear
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
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CX067711/c
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/clone_lib="Stanley Frontal SN pool 2"
/note="Organ: brain; Vector: pGR2.1-TOPO (Invitrogen);
Site_1: EcoN N; Total RNA (purified with Trizol and DNAsed
before use) was reverse transcribed using a modified
oligo-dT primer containing Real and HindIII sites.
Double- stranded cDNA was digested with Real, resulting in
blunt ended cDNA was split into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor.
S'-TCAGGCGCCCCGGGCAGGT-3' or 5'-
AGGCGTGGTGCGCAGGGAGGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select
CDNA subtraction kit. Pool of two schizophrenics, male age
44 and female age 56 (S-116, S-118) subtracted by pool of
two mentally normal male individuals ages 41 and 53
(S-124, S-141). Tissues were obtained from the Stanley
Neuropathology Consortium (www.stanleylab.org). Library
constructed and subtracted by Dr. Nancy Johnston [(410)
614-3918, nlj@welchlink.welch.jhu.edu]."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with Plate: FQY8071 row: A column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 27; DB 1;
100.0%; Pred. No. 0.085;
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: FQY8071 row: A column: 24
Seg primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="MARC 6BOV"
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/lab_host="DH108"
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Best Local Similarity 100.
Matches 27; Conservative
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DEFINITION
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PEATURES

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CXU67711 733 bp mRNA linear EST 03-JAN-2005 1322352 NCCCWA 04RT Oncorbynchus mykiss cDNA, mRNA sequence. CX067711
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Rexroad,C.E., Rise,M., Koop,B., von Schalburg,K. and Yao,J. 04RT grool, NCCCWA/WVU EST Project, Phase II, in collaboration with GRASP
                                                                                                                                                                                                                                                                        AL718806 AL718806 AL718806 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA CIONE BNOAA037ZE05 3', mRNA sequence.
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( bases I to 609)

Coimbra, R., Well, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)
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/dev stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
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Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
Gaps
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Oncorhynchus mykiss
                                                            1132 GACTCATCCTTCCAGGGCACCGACACA 1158
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                                                                                               133 GACTCATCCTTCCAGGCACCGACACA 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA037ZE05"
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27; Conservative
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    Matches
                                                                                                                                               RESULT 70
DN615123/c
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BF043991
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                                                                                                                                                                                                                                            /unl_type="mRNA"
/ub xref="taxon:802"
/lab host="rop10"
/lab host="rop10"
/clone lib="NQCCOr. QRR"
/note="Vector: pCR 4-TOPO; This is an early neurogenesis
SSH library created by Mathew L. Rise constructed by
subtracting late neurogenesis (mixed stages: hindbrain
swelling + heart tube with peristalsis) from early
neurogenesis (mixed stages: neural groove + 1/2 epiboly).
Fish were from a domesticated strain (Spring Valley Trout
Farm, Langley, B.C.), courtesy of Bob Devlin, DFO. These
are mostly internal (coding) sequences."
                                                          Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
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(bases 1 to 738)

(colmbra, W. Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardellin, J. P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)
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/db_xref="taxon:7955"
/clone="BNDAA025211"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers
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100.0%; Pred. No. 0.088;
tive 0; Mismatches 0; Indels
    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rerio cDNA clone BNOAA025ZB11 3', mRNA sequence.
  Kearneysville, WV 25430,
                                                                                                                                                                                                              1. .733
/organism="Oncorhynchus mykiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="subtracted cDNA library"
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Seg primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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11876 Leetown Road, Kean
Tel: 304 724 8340 x2129
Fax: 304 725 0351
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Danio rerio
                                                                                                                           cross_match v0.990329.
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Unpublished (2002)
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Best Local Similarity
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ORGANISM
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AL717228/c
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1.6%; Score 27; DB 1; 100.0%; Pred. No. 0.088;

Query Match Best Local Similarity

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/clone="PSCACCI3"
/tissue type="Whole embryos excised from megagametophytes"
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/lab_hoft="Whole"
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/clone lib="Subtracted pine embryo library, Lib B"
/clone lib="Subtracted pine embryo sorticled in
realization: Site_1: Spei; Library enriched in
transcripts present in early phase of lobholly pine embryo
maturation. A subtractive library was made using the
protocols of Clontech (Palo Alto,CA). RNA from loblolly
pine embryos in which cotyledons had just emerged (Stage
9.1, see Ciavatta WT, Morillon R, Pullman GS, Chrispeels
M, Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of lobholly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
[http://www.plantphysiol.org/cgi/content/full/127/4/1556])
was subtracted from RNA from pine embryos collected two
weeks after cotyledon emergence (Stage 9.3)."
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BP250022B20H1 Soares normalized bovine placenta Bos taurus CDNA
Glone BP250022B20H1 5', mRNA sequence.
BP043991
                                                                                                                                                                                                                               EST 21-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: C. Robin Buell
Plant Genomics Group
The Institute for Genomic Research
P3712 Medical Center Dr. Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: M13 forward.
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Buell, C.R., Zheng, L., Cowles, A. and Cairney, J.

Sequencing of BSTs from loblolly pine embryonic libraries
Unpublished (2004)
                                                                                                                                                                                                                                                          EST968173 Subtracted pine embryo library, Lib_B Pinus taeda cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/culfivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
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100.0%; Pred. No. 0.088;
iive 0; Mismatches 0; Indels
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1687 TTGTAAGTACCTCGGCCGCGACCACGC 1713
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/organism="Pinus taeda"
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                                                             30 rigiaAgraccicescesesece
                                                                                                                                                                                                                                                                                                clone PSACC13, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                          DN615123.1 GI:61672623
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EST 26-NOV-2002
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/mol type="mNNA"
/db xref="taxon.4565"
/dclone="wri2e:pk008.e13.f"
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1 (bases 1 to 232)
Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
Expressed sequence tags from soybean root hair subtractive cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.
Miao, G., Caraher, N. and Hanafey, M.K.
Unborbt Wheat CDND Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
I Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2607
Pax: 302-631-2607
Pax: 302-631-2607
Pax: 302-631-2607
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Pax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: root hairs; Vector: pGEM-T-Easy; cDNA ogenerated from soybean root hair tissue treated with Bradyrhizobium japonicum for 6 hours."
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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                                                                                                                         Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-884-0588
Email: staceyg@missouri.edu
Single pass sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Matches 26; Conserv
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewinGuliuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Febearch Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
Phis sequence is vector free and at least 200 bp in length.
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/lab host="DH10B"
/clone lib="Soares normalized bovine placenta"
/clone lib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pT713Pac; Site_1: BcoRI;
Site_2: NotI; The cDNA library was contrributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Beoras; Bovidae; Bovinae; Bos.
1 (bases 1 to 206)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Lewin, H. A. W. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 206 Std Error: 0.00
Plate: BP250022B20 row: H column: 1
Seq primer: AGCGGATAACAATTCACAGGA
High quality sequence stop: 206.
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/db_xref="taxon:9913"
/clone="BP250022B20H1"
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   GI:10761046
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Unpublished (2000)
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Matches 26; Conservative
                                                                   Bos taurus (cow)
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   BF043991.1
                                                                                                    Bos taurus
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ag65e01.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone
IMAGE:2035800, mRNA sequence.
                                                                                                                                                                                                                                                                            AL726074 2255 bp mRNA linear EST 18-APR-2002 AL726074 Danio rerio embryonic inner ear subtracted cDNA Danio rereio cDNA clone BN0AA080ZD03 5', mRNA sequence. AL726074
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1 (Dases 1 to 255)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Weissenbach,J. and Petit,C.

8 subtracted cDNA library from the zebrafish (Danio rerio) embryonic inner ear Unpublished (2002)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 288)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="embryonic"
| clone_lib="Danio rerio embryonic inner ear subtracted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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                                                         Length 232;
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                                                                                                 0; Indels
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                                                     1.5%; Score 26; DB 6;
100.0%; Pred. No. 0.26;
iive 0; Mismatches
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comparable uninfected leaves"
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                                                                                                                                        1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                             205 TGTAAGTACCTCGGCGGCGACCACGC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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                                                                            Best Local Similarity 100.
Matches 26; Conservative
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/downer="Invage: 201800"
/clone="Invage: 201800"
/tissue_type="frontal lobe (see description)"
/tissue_type="frontal lobe (see description)"
/lab host="DH108 (phage-resistant)"
/clone lib="Stanley Frontal SN pool 2"
/note="Organ: brain, Vector: pCR2.1-TOPO (Invitrogen);
Site_1: ECORI; Total RNA (purified with Trizol and DNAsed before use) was reverse transcribed using a modified oligo-dT primer containing Rsal and HindIII sites.
Double- stranded cDNA was digested with Rsal, resulting in blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is set the driver, the other set was split in half again and each half linked to a different adaptor
(5'-TCGAGCGCGCCGCGCGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select cDNA authraction Kit. Pool of two schizophrenics, male age two mentally normal male individuals ages 41 and 53 (S-116, S-118) subtracted by pool of two mentally normal male individuals ages 41 and 53 (S-124, S-141). Tissues were obtained from the Stanley constructed and subtracted by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu]."
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1 (bases I to 344)

1 (bases I to 344)

1 (bases I to 344)

Mao, G., Caraher, N., Molters, P., Dolan, M., Hainey, C., Yuan, Z., Mao, G., Caraher, N. and Hanafey, M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco
High quality sequence stop: 287,
Location/Qualifiers
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Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
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/db_xref="taxon:9606"
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CA734840
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Best Local Similarity
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1 (Dassellova, 1402)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Pahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                 /clome_lib="wpiis"
/note="Vector: PGEM-T Easy; Site 1: Smal; Wheat, Polk
cultivar (resistant), infected with septoria tritici
strain A 24 hours after infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
E. I. DuPont de Nemours and Company
1 Innovation Way,
1 F.O. Box 6104, Newark, DE 19714-6104, USA
1 Innovation Way,
1 Fai: 302-631-2607
Fax: 302-631-2607
Email: Scott. V. Tingey@USA.dupont.com
Seq primer: Ml3.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Score 26; DB 6; Length 344;
100.0%; Pred. No. 0.27;
tive 0; Mismatches 0; Indels
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Fax: 402 762 4390
                                                                                                                                                             /organism="Triticum aestivum"
                                                                                                                                                                              /mol_type="mRNA"

db_xref="taxon:455"

/clone="wpile.pk002.ell"

/tissue_type="leaf"

/lab_host="DH108"
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/db xref="taxon:9913"
/tissue_type="pooled"
/lab host="bH108"
/clone_lib="WARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
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Seg primer: ATTTAGGTGACACTATAG.
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BACKWARD: GTTTTCCCAGTCACGACG
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PCR PRimers
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VERSION
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LOCUS
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                BF150866 425 bp mRNA linear EST 29-DEC-2000 uy88910.yl NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666690 5',
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/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Gligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentía;
Sciurognathi; Muroidea; Muridae; Mus.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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                                                                                                                                       1.5%; Score 26; DB 1; Length 402; ilarity 100.0%; Pred. No. 0.27; Conservative 0; Mismatches 0; Indels
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/dev_stage="7 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
0.27;
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/strain="mix PNB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3666690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 26; DB
100.0%; Pred. No. 0.2
ive 0; Mismatches
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .425
/organism="Mus musculus"
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High quality sequence stop: 395.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                       68 GAAGCAGIGCCCACTCIGGCICCTCC 93
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Unpublished (1997)
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Best Local Similarity 100.
Matches 26; Conservative
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BF150866
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SECTION 485 bp mRNA linear EST 20-DEC-2002 SEMDIGO Rice callus and differential tissue SSH library Oryza eativa cDNA, mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                         1. .475
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="texon:10116"
/clone="srcs1-00007-e10"
/tissue type="Cornea"
/clone_lib="srcs1 (10883)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Site_2: EcoRI;
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/culTivar="Muyunjing No. 7"
/culd_xref="xxon:4530"
/clone_lib="Rice callus and differential tissue SSH
                                                                                                           Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00007 row: e column: 10.
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100.0%; Pred. No. 0.28;
ive 0; Mismatches 0; Indels
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Du,X., Wang,D. and Yang,J.
Rice cDNA from callus (2002)
Unpublished (2002)
Contact: DU Xiling
Institute of Genetics, Fudan University
Handan Road 220, Shanghai 200433, China
Tel: 86-21-6564-3715
Email: dxiling@yahoo.com.cn.
Location/Qualifiers
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1 (bases 1 to 475)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
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Best Local Similarity
Matches 26; Conserv
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JOURNAL
COMMENT
                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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AMGNNUC:SRCS1-00007-E10-A grcs1 (10883) Rattus norvegicus cDNA clone srcs1-00007-e10 5', mRNA sequence.
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/note="Torgan: mammary; vector: pCMV-SPORT6; Site 1: SalI;
/note="Torgan: mammary; vector: pCMV-SPORT6; Site 1: SalI;
/note="Cramary; vector: pcm, primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                              AW762557 426 bp mRNA linear EST 04-MAY-2000 ur57f12.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3154415 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
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Sukaryotas, Metazotas, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                            1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Other ESTB: ur57f12.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 GATGTTAAGCTCAAAGGCATCCCTGT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 GATGITAAGCICAAAGGCATCCCTGT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: -40RP from Gibco
High quality sequence stop: 422.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:3154415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB732455.1 GI:29799612
                                                                                                                                       AW762557.1 GI:7694486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Conservative
                                                                                             mRNA sequence.
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DEFINITION
                                                               DEFINITION
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CB732455
                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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    RESULT 79
                         AW762557
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us-09-989-890-105.oligo.rst

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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                RESULT 84
AI267373/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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JOURNAL
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KEYWORDS
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                                      CF036397 501 bp mRNA linear EST 17-JUL-2003
QCG30h07.yg QCG Zea mays cDNA clone QCG30h07, mRNA sequence.
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(Combra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C. and Petit, C. embryonic inner ear Unpublished (2002)
                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta; Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. 1 (bases 1 to 501) Genoplante.
                                                                                                                                                                                                                                                                   Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                            This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Genoscope Gentre National de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.5%; Score 26; DB 6; Length 501; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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/clone="QCG30h07"
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/clone_lib="QCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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                                                                                              CF036397.1 GI:32931585
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Danio rerio
                                                                                                                                      Zea mays
                                                                                                                                                           Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                     DEFINITION
ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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RESULT 82
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かんはますり

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/d_one="Intage :03566"
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//Lone="Intage :03566"
//Lissue type="frontal lobe (see description)"
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//Lone lib="Stanley Frontal SN pool 2"
//Lone lib="Stanley Frontal SN pool 2"
//Lone lib="Stanley Frontal SN pool 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 543)

1 (bases 1 to 543)

1 (laster Hono.M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,M., Lemon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Trheising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)

Contact: Wilson RK
                                  /tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from 61050 consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 bp mRNA linear EST 17-NC aq64c09.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035696, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                     /note="subtracted cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.5%; Score 26; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches
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ORIGIN

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AL714414 Amio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA Danio rerio cDNA Clone BNOAA005ZH12 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 557)
Coimbra, K. Weil, D., Brottier, P., Blanchard, S., Levi, M.,
Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conference: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                     Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                           Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

(Cypriniformes; Cyprinidae; Danio.

(Coimbrac, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J. P., Weissenbach, J. and Perit, C.

a wubtracted cDNA library from the zebrafish (Danio rerio) ambryonic inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 26; DB 1; Length 557;
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.00.0%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="subtracted cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.2 Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      1. .557
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/clone="BNOAA003ZC08"
/tissue_type="inner ear"
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/clone="BNOAA005ZH12"
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         Danio rerio
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1 (bases I to 547)

Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries UNDA, ARS, US Meat Animal Research Center
Po Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Pax: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: LAMB004 row: M column: 8
Seq primer: TAGAAGGCACAGTCGAGG.
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AL714240 GI:20178843
EST. EST. 18-APR-2002
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constructed and subtracted by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu]."
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                                                                                                                                                                                                                                                                                                                                                         CB464871 547 bp mRNA linear 726118 MARC 6BOV Bos taurus cDNA 3', mRNA sequence
                                                                                                                                                0; Indels
                                                                                                Query Match 1.5%; Score 26; DB 1; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 26; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9913"
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/lab_host="DH10B"
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AL714240/c
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AL716984 Danio rerio embryonic inner ex subtracted cDNA Danio rerio cDNA clone BNOAA021ZAO1 5', mRNA sequence.
AL716984 Danio EN0AA021ZAO1 5', mRNA sequence.
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1 (bases 1 to 572)
2 (colmbra, W. Well, D., Brottier, P., Blanchard, S., Levi, M., Hardellin, J. P., Neissenbach, J. and Perit, C. A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                   /organism="Danio rerio"
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/clone="BNOMAO032C08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
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/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
           Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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1.5%; Score 26; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:7955"
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AL714276 AL714276.1 GI:20178879
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1 (Dases 1 to 558)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Aradelin,J.D., Weissenbach,J. and Petit,C.
A subtracted CDNA library from the zebrafish (Danio rerio)
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1 (bases 1 to 561)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Weissenbach,J. and Petit,C.

A subtracted cDNA library from the zebrafish (Danio rerio)
Contact: Genoscope
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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100.0%; Pred. No. 0.28;
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             Pred. No. 0.28;
100.0%; Prec. ...
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Local Similarity 100.0%; Pred. No. 0.2
Best Local Similarity 00.0%; Mismatches
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/db_xref="taxon:7955"
/clone="BNOAA005ZH12"
/tissue_type="inner ear"
                                                                      1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                 /organism="Danio rerio"
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      Best Local Similarity 100.
Matches 26; Conservative
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Fax: 81-45-50/3216

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hizozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kadawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Salto,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Watahiki,A., Muramateu,M. and Hayashizaki,Y.
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequence Mam. Genome. 12, 673-677 (2001)

Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia real-time sequence Science Laboratory in Riken
Genomic Sciences Center and Genome Exploration Research foroup in Riken
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Savolan, M., Zhu, Y., Zimer, A., Yang, E., Carninci, P., Gakazume, N., Hirozane-Kishikawa, T., Komo, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Arakwa, T., Fukuda, A., Harahizume, W., Imocani, K., Ishii, Y., Arakwa, T., Kukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Shinagawa, A., Yasunishi, A., Sakai, K., Sasai, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-509-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Figures were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, adult inner ear"
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/tissue_type="inner ear"
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/strain="C57BL/6J"
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Sciutognathi; Muroidea; Murinae; Mus.

1 (Dases 1 to 657)

Sokazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Obatco,N., Saito,R., Suzuki,H., Yamanaka,I., Kriyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Corbani,L.B., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Glaminold,M., Gissi,C., Godzik,A., Gough,J., Garimon,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKelais,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pescole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachadran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ringyald,M., Schneider,C., Semple,C.A., Secou,M., Shimada,K., Suhmada,K., Suhtana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY753126 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930111008 5', mRNA sequence.
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                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.ft).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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             QCU9g04.yg QCU Zea mays cDNA clone QCU9g04, mRNA sequence.
CF064307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="seedling minus kernel"
/clone_lib="QCU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="f333 or f334"
/db_xref="taxon:4577"
/clone="QCU9g04"
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Mus musculus
                                                                             GI:33104347
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KEYWORDS
SOURCE
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/clone="!tMAGE:5341085"
/clone="!tMAGE:5341085"
/tissue_type="tumor, gross tissue"
/dev stage="tumor, gross tissue"
/dev stage="10 months"
/lab_host="DH10B"
/clone=lib="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                                                                                                                                           E 1 (bases 1 to 680)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inh.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llhl.gov

Plate: LLAM11866 row: g column: 06

High quality sequence stop: 676.
BI653517 680 bp mRNA linear EST 12-SEP-2001
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602903535F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5033097 5',
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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100.0%; Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
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                                                       mRNA sequence.
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Cramer, R.A., Craven, K.D., Thon, M.R., Cho, Y., Knudson, D.L., Mitchell, T.K. and Lawrence, C.B.
Expressed Sequence Tag (BST) Analysis of a Compatible Alternaria brassicicola-Brassica oleracea Interaction
Unpublished (2005)
Contact: Dr. Thomas K. Mitchell
Contact: Dr. Thomas K. Mitchell
Contact: Dr. Thomas K. Mitchell
Research, NC State University
B51 Main Campus Dr. Suite 233, Raleigh, NC 27606, USA
Tel: (919) 513-026
Fax: (919) 513-024
Email: thomas mitchell@ncsu.edu
Seq primer: T7 SF6 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mamorary vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DN478595 692 bp mRNA linear EST 09-MAR-2005 altr010xm17 A. brassicicola mycelial culture infecting B. oleracea Alternaria brassicicola cDNA clone altr010xm17, mRNA sequence.
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Alternaria brassicicola
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Dothideomycetes,
Pleosporales, Pleosporaceae, mitosporic Pleosporaceae, Alternaria.
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     Ph.D.
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/clone_lib="A. brassicicola mycelial culture infecting
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng I CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov. f column: 10 Plate: LLAMI1092 row: f column: 10 High quality sequence stop: 685. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:5033097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.2 Matches 26; Conservative 0; Mismatches
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/clone="altr010xm17"
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/strain="ATCC 96866"
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Query Match
Best Local Similarity 100.03
Matches 26; Conservative
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CDNA, mRNA sequence.
CV943849
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Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.

1 (bases 1 to 707)

Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Mindass,J., Binder,A., Bizch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Judelson, H.S.
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24 degrees C, minimal media minus Nitrogen. Infecting
Brassica oleracea Var. Capitata cultivar 'tendersweetFl'"
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/note="Vector: pSPORT1"
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                                                                      Length 692;
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15782637
Contact: Judelson HS
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/mol_type="mRNA"
/strain="88069"
                                                                      1.5%; Score 26; DB 8;
100.0%; Pred. No. 0.29;
vative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
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                                                                                                                                                               28 TGTAAGTACCTCGGCCGCGACCACGC 3
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Mus musculus (house mouse)
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM1284 row: e column: 05
High quality sequence stop: 720.
I. 722
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1 (Dases I to 737)

Randall, T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C.,
Randall, T., Dwyer, R.A., Huitema, E., Beyer, K., Yottchick, Gaffney, T.,
Iaw, M., Testa, A., Tortc-Alalibo, A., Zhang, M., Zheng, L.,
Muhdass, J., Binder, A., Birch, P.W.; Gisi, U., Govers, F., Gow, N.A.,
Mauch, F., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S.,
Iam, S. T. and Judelson, H.S.
Liarge-scale gene discovery in the comycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Goiurognathi; Muroidea; Muridae; Musinae; Mus. 1 (bases 1 to 722)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
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Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
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100.0%; Pred. No. v.
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CV944323.1 GI:58134079
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Gaps

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
DNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
EDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 746.
       Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Contact: Robert Strausberg, Ph.D.
Email: cgapDs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
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cDNA Library Preparation: Life Technologies, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
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Location/Qualifiers
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Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 746)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mol. Plant-Microbe Interact. 18 (3), 15782637
Contact: Judelson HS
Contact: Judelson HS
University of California
Webber Hall, Riverside, CA 92521, US
Fax: 909 787 4199
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US-09-551-621A-76 US-10-076-622-76 US-09-902-540-1273 US-09-284-782-11	US-09-323-873A-27	US-10-027-807-7	US-10-027-807-10	US-10-027-807-16	US-09-961-058-7	US-US-961-US8-9 US-10-010-667A-27	US-10-116-437A-7	US-10-116-437A-10	US-10-116-437A-13	US-10-116-437A-16 TIS-09-404-8793-242	US-09-338-933-242	US-09-215-681-242	US-09-216-003A-242	US-US-66/-65/-242 TIS-10-198-053-343	US-09-827-271-242	US-09-323-873A-24	US-09-455-486-25	US-10-027-807-3	US-US-333-716-3 TIS-10-010-6678-24	US-10-116-437A-2	US-09-284-782-6	US-09-404-879A-304	US-09-338-933-304	US-US-ZIS-68I-304 IIS-09-216-0032-304	US-09-667-857-304	US-10-198-053-304	US-09-827-271-304	US-09-404-879A-201 US-09-338-933-201	US-09-338-333-201 US-09-215-681-201	US-09-216-003A-201	US-09-667-857-201	US-10-198-053-201	US-09-82/-2/1-201 US-09-404-879A-293	US-09-338-933-293	US-09-215-681-293	US-09-218-003A-293 US-09-667-857-293	US-10-198-053-293	US-09-827-271-293	US-US-404-8/9A-185 IIS-09-338-933-185	US-09-215-681-185	US-09-216-003A-185	US-09-667-857-185	US-10-198-053-185 US-08-827-271-185	US-09-221-298-57	US-09-401-064-57	US-09-222-575-122	US-09-389-681-122	US-US-620-403B-122 IIS-09-339-338-122	US-09-433-826B-122	US-09-604-287A-122	US-09-285-480-122	US-09-834-759-122 US-09-590-751A-122	US-09-551-621-122	US-09-551-621A-122	US-10-076-622-122
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150 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCGG 209 121 CGCACCCGTAGACCCAAGAGCCTGGCCACCATGGCCATGAGCATTACCTTC 180	
	QY 1261 GGACCAGGAACCCCTGTGGGAGAGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCC 1320
TGGGTGTGGGGGGGGGGGGGTTCTGCTTCCGCCGGGGGGG	Qy         1321 TGCCTTGGCTGACTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC         1380
CGCTGTCGAGCCTGTGTGCGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG	Ay 1381 TCCTTGCATCCCAGCTGGTCTGATCCCTGCCAGGGCCCCTTCCTT
GGGACTGCTGAAGCCAACTGGGCCAAGGGCCAATGGAGTGCCCCCCAGCCCTGATCGT	Oy 1441 TCACGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 1500 
21 GCACCCCCAGCCGGCGGATGGCCCAGGCCCCAGGCCCCCAGGCCCCCCTCAGGCAGG	Qy 1501 ACTCCATCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCTCC
TACCCGATGTTAAGCTCAAAAGCATCCCTGTGTATCCCTACCCGAAGGGCCACTCCCCA	QY         1561         TCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATT
GCCCCTGATGGGGACTCCTGCTGCAAGAGGCATGCCGCACCCCATGGACAC	Oy 1621 CTATGTTATGTTAAGGAGTTGGTTCTTGGCTGATGTTCTGTATCTTAACATGAC 1680
AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT	Oy 1681 CACAGTTTGTAAGTAC 1696
661 GAGTCGGACCTGGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720 	RESULT 2 US-10-131-827-8473 ; Sequence 8473, Application US/10131827
721 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC 780	
781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 840 	; APPLICANT: Woodward, Robert ; APPLICANT: Ly, Ngoc ; TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE ; TILLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES ; TILLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGGGGC 900	
901 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 960 	
961 ACTCGGGCTGCCCCAACCGCTGCTGCCCTGACGTGGCCCATGAGACCATGGTGGGC 1020 	; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 4473 ; LENGTH: 224 ; TYPE: DNA
1021 TCAGGTCTCAGCCAGGATGAGCTGACAGATCTCCCAGGAGACGACTGCCAGATGCC 1080	OKGANLSM: HOMO Baplens FEATURE: NAME/KEY: misc feature LOCATION: (1) (224)
1081 ATGGCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC   140	A, C,
1141 TTCCAGGGCACCCGACACACACGCTCGGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC 1200	Similarity 100.0%; Pred. No. 0.064; 5; Conservative 0; Mismatches 0; Indels
1230 TTCCAGGGCACCGACCACAGACTCGTCGGGGGCACCCTTGCTCCAGGTGTACTGCTGACCC 1289	Qy 1689 GTAAGTACCTCGGCCGCACCACGC 1713

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APPLICANT: Sharel, Johnny
APPLICANT: Astel, John H.
APPLICANT: Astel, John H.
APPLICANT: Bedege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
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APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 246
LINGTH: 482
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSUCTS THAT
TITLE OF INVENTION: 3820,002/200130 463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
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LENGTH: 483
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100.0%; Pred. No. 0.61;
iive 0; Mismatches 0; Indels
   1.3%; Score 23; DB 3; Length 468; 100.0%; Pred. No. 0.61; cive 0; Mismatches 0; Indels
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Sequence 239, Application US/09328475C
; Patent No. 6476207
GENERAL INPORMATION:
                                                                                                                                                                                        104 AAGTACCTCGGCCGCGACCACGC 82
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-239
Query Match
Best Local Similarity 100.0
Matches 23, Conservative
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LY, MOOMALIN, MOOMED AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT FILING DATE: 2002-09-06
PRIOR PILING DATE: 2001-00-22
PRIOR FILING DATE: 2001-00-22
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 8150
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US-09-128-475C-111/C

US-09-128-475C-111/C

Sequence 111, Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy

APPLICANT: Endeq, Wilson O.

APPLICANT: Endeq, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Wilson O.

APPLICANT: Schlegel, Wilson O.

APPLICANT: Schlegel, Wilson O.

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: AEE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TITLE REFERENCE: 1532.002/200130.463

TITLE OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 111

EMBORTH: 468

TUDE OF INVENTION: ARE BEREAUTH AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND G
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                                           Graderaccredecedecedece 213
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                                                                                                                                                                                                                 Sequence 8150, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: (1)...(170)
; OTHER INFORMATION: N = A, T, C or G
US-10-131-827-8150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo Sapien
                                                                                                                                                                             US-10-131-827-8150
                                              189
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(499)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo Sapien
                                                                                  ; CIRBR 1328-475C-185
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APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John B.
APPLICANT: Steinman, Vahn E.
APPLICANT: Steinman, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
CURRENT FILING DATE: 1999-06-09
SOFTWARE: PastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                             Gaps
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APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathlen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFREENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
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                         DB 3; Length 483;
0.61;
                                                                          0; Indels
                    1.3%; Score 23; DB 100.0%; Pred. No. 0.6 tive 0; Mismatches
                                                                                                                        1691 AAGTACCTCGGCCGCGACCACGC 1713
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US-09-328-475C-224/c
i Sequence 224, application US/09328475C
i Patent No. 6476207
                                                                                                                                                    104 AAGTACCTCGCCGCGACCACGC 82
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Sequence 185, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-224
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Actel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
                                                Local Similarity 100. hes 23; Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Matches
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; Sequence 181, Application US/09328475C
; Patent No. 6476207
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Carroll III, Eddie
; APPLICANT: Bradege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Ford, Donna M.
; APPLICANT: Science, Wilson O.
; APPLICANT: Science of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of 
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APPLICANT: Zhang, Jimmy
APPLICANT: Astel, John
APPLICANT: Astel, John
APPLICANT: Bridge, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Stelmann, Kathleen E.
ITILE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
ITILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
FURRENT APPLICANTION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
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     DB 3; Length 499;
0.61;
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Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches (
Query Match
1.3%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 23; Conservative 0; Mismatches
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8-09-138-475C-196/c
; Sequence 196, Application US/09328475C
; Patent No. 6476207
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NAME/KEY: misc feature
LOCATION: (1)...(501)
OTHER INFORMATION: n = A,T,C or G
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Gaps

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APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSIATE CANCER
FILE REFRENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 277
LENGTH: 724
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 315
LENGTH: 72
TYPE: DNA
ORGANISM: Homo Sapien
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; Sequence 277, Application US/09128475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Actel, Jon APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1691 AAGTACCTCGGCCGCGACCACGC 1713
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Patent No. 6476207
GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 AAGTACCTCGGCCGCGACCACGC 73
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NAME/KEY: misc_feature

LOCATION: (1)...(722)

OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc feature
LOCATION: (1)...(724)

OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-328-475C-295
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US-09-328-475C-305/c
| Sequence 316, Application US/09328475C
| Patent No. 6476207
| GENERAL INFORMATION:
| APPLICANT: Zahaq, Jimmy |
| APPLICANT: Aptel, John H.
| APPLICANT: Endege, Wilson O. |
| APPLICANT: Ford, Donna M. |
| APPLICANT: Schiegel, Robert |
| APPLICANT: Schiegel, Robert |
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| APPLICANT: Schiegel, Robert |
| APPLICANT: Schiegel, Robert |
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| APPLICANT: Schiegel, Robert |
| APPLICANT: Schieg
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APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert.
APPLICANT: Schlegel, Robert.
APPLICANT: Stelnmann, Yathleen E.
APPLICANT: Stelnmann, Kathleen E.
APPLICANT: Stelnmann, Kathleen E.
APPLICANT: Stelnmann, Kathleen E.
                                                                                                                                                                                                                                                                                                                                                                                    Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.3%; Score 23; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches
                    SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 196 LENGTH: 511
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US-09-328-475C-315/c
| Sequence 315, Application US/09328475C
| Patent No. 6476207
| GENERAL INFORMATION:
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                                                                                                                                                                               FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(511)

OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-305
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Best Local Similarity 100.
Matches 23; Conservative
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                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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TYPE: DNA
ORGANISM: Homo Sapien
PEATURE:
NAME/KEY:
LOCATION: (1)...(736)
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APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Carroll III, Eddie
APPLICANT: Bridge, Wilson O.

APPLICANT: Bridge, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Research
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: AND STATE 1999-06-09

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 329

LENGTH: 725
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John B.
APPLICANT: Schiegel, Robert
APPLICANT: Schiegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 295
LENGTH: 725
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100.0%; Pred. No. 0.61;
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Sequence 329, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
US-09-328-475C-331/c
; Sequence 331, Application US/09328475C
; Patent No. 6476207
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; LCCATION: (1)...(725)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-295
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i_LOCATION: (1)...(725)
cTHER INFORMATION: n = A,T,C or G
US-09-328-475C-329
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Best Local Similarity 100.(
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
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APPLICANT: Astel, John H.

APPLICANT: Astel, John H.

APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ASE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SERGIA DATE: 1991-04-05
TYPE: NOT-
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GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.

APPLICANT: Garroll III; Eddie
APPLICANT: Budege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Mondan, John E.

APPLICANT: Steinman, Kathleen E.

APPLICANT: Steinman, Kathleen E.

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: QUBERENTIALLY REGULATED IN PROSTATE CANCER

TITLE OF INVENTION: 1999-06-09

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 294

LENGTH: 736
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1.3%; Score 23; DB 3; Length 727;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(727)
CTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-294
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1691 AAGTACCTCGGCCGCGACCACGC 1713
1691 AAGTACCTCGGCCGCGACCACGC 1713
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                                                                                              124 AAGTACCTCGGCCGCGACCACGC 102
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8-09-328-475C-330/c
; Sequence 330, Application US/09328475C
; Patent No. 6476207
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LOCATION: (1)...(744)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(741)
OTHER INFORMATION: n = A,T,C or G
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Matches 23; Conservative
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ORGANISM: Homo Sapien
FEATURE:
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US-09-328-475C-276/c
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GENERAL INFORMATION:

APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Endege, Wilson O.

APPLICANT: Endege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlagel, Robert
APPLICANT: Schlagel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENES AND GENES
TITLE OF INVENTION: QUARRER: US/09/328, 475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOCTWARER FALESE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FASTERE FAST
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100.0%; Pred. No. 0.61;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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                                    US-09-328-475C-314/c
; Sequence 314, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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US-09-328-475C-304/c
; Sequence 304, Application US/09328475C
; Patent No. 6476207
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-314
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-304
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Best Local Similarity 100.
Matches 23; Conservative
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Best Local Similarity 100.
Matches 23; Conservative
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Sequence 276, Application US/09328475C

Sequence 276, Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:

APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Garroll III, Eddie

APPLICANT: Garroll III, Eddie

APPLICANT: Bridge, Wilson O.

APPLICANT: Monahan, Oblu E.

APPLICANT: Monahan, Oblu E.

APPLICANT: Steinmann, Kathleen E.

APPLICANT: Steinmann, Kathleen E.

TITLE OF INVENTION: GRABE SAND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER

TITLE OF INVENTION : ARE DIFFERENTALLY REGULATED IN PROSTATE

CURRENT PELING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 276

SEQ ID NO 276

LENGTH: 744
GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Zhang, Jimmy
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Budege, Wilson O.
APPLICANT: Bradege, Wilson O.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENER AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NOWER: 1999-06-09
KUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 330
LENGTH: 741
TYPE: DNA
CORGANISM: HOMO Sapien
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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Gaps

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Sequence 268, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SSOFTWARE: PatentIn Ver. 2.0
SSOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Achiegel, Robert
APPLICANT: Schiegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 153
SEQ ID NO 153
LENGTH: 780
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0.61;
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                                                                                                                                                                                  DB 3;
                                                                                                                                                                               Query Match
1.3%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                      1691 AAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                                                          86 AAGTACCTCGGCCGCGACCACGC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AAGTACCTCGGCCGCGACCACGC 85
                                                NAME/KEY: misc_feature

i LCCATION: (1)...(772)

CTHER INFORMATION: n = A,T,C or G

US-09-328-475C-158
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| LOCATION: (1)...(780)

| OTHER INFORMATION: n = A,T,C or G

US-09-328-475C-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
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ORGANISM: Homo Sapien FEATURE:
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Nohn E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Nohn E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ABE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REPERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SSPTWARE: FastSEQ for Windows Version 3.0
SERVICENT: NANA
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinman, Kathleen E.
TITLE OF INVENTION: GRENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GRENES AND GENE EXPRESSION PROSUCTS CANCER
FILE REFERENCE: 1532.002/20130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT PILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE FESTSEQ for Windows Version 3.0
                                                                                                         Gaps
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                                                   1.3%; Score 23; DB 3; Length 744;
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100.0%; Pred. No. 0.61;
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                                                                                 0.61,
                                              Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                           RESULT 22
US-09-328-475C-328/c
Sequence 328, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
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US-09-128-475C-158/c
'S Sequence 158, Application US/09328475C
'Patent No. 6476207
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(747)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo Sapien
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Matches 23; Conserv
US-09-328-475C-276
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LENGTH: 747
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TYPE: DNA
ORGANISM: Homo Sapien
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US-09-128-475C-167/C

Sequence 167, Application US/09328475C

Patent No. 647207

GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy

APPLICANT: Astel, Jill, Eddie

APPLICANT: Endege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE

CURRENT APPLICATION WUMBER: 1959-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 167

SEQ ID NO 167

LENTH: 797
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US-09-328-475C-229/C
US-09-328-475C-229/C
; Sequence 229, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Astel, Jonn H.
; APPLICANT: Astel, Jonn H.
; APPLICANT: Ford, Donna M.
; APPLICANT: Ford, Donna M.
; APPLICANT: Schlegel, Robert
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
; TITLE OF INVENTION: 483
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
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100.0%; Pred. No. 0.61;
ive 0; Mismatches 0; Indels
                                                                                                             DB 3; Length 781;
0.61;
                                                                                                           Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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NAME/KEY: misc_feature
LOCATION: (1)...(781)
OTHER INFORMATION: n = a, t, c or g
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OTHER INFORMATION: n = A,T,C or G
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Matches 23; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-328-475C-167
                                                                    US-09-280-116-268
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APPLICANT: Zhang, Jimmy
APPLICANT: Actal July
APPLICANT: Actal July
APPLICANT: Actal July
APPLICANT: Badege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Bridge, Wilson O.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
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APPLICANT: Schlegel, Robert
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APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
CURRENT SPINGANTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
CURRENT PLING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 240
LENGTH: 815
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert.
APPLICANT: Stelingel, Robert.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
                                                                                                                                                                                                                                                                                                                                                     0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 229 LENGTH: 815
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US-09-328-475C-249/c
US-09-328-475C-249/c
; Sequence 249, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              82 AAGTACCTCGGCCGCGACCACGC 60
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; Sequence 240, Application US/09328475C
; Patent No. 6476207
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NAME/KEY: misc_feature
LOCATION: (1)._.(815)
OTHER INFORMATION: n = A,T,C or G
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COTHER INFORMATION: n = A,T,C or G
US-09-328-475C-229
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APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
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Best Local Similarity 100.0
Matches 23; Conservative
                                                                            TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: misc feature
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APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REPREBROE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: PREISEQ FOR Windows Version 3.0
SOFTWARE: PREISEQ FOR Windows Version 3.0
TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.3%; Score 23; DB 3; Length 829; Best Local Similarity 100.0%; Pred. No. 0.61; Matches 23; Conservative 0; Mismatches 0; Indels
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; Sequence 43, Application US/09328475C
; Patent No. 6476207
                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-191
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (1)...(829)
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ORGANISM: Homo Sapien
FEATURE:
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US-09-328-475C-245/C
; Sequence 245, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: ZAnag, Jimmy
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Schlegel, Robert
; APPLICANT: Schlegel, Robert
; APPLICANT: Schlegel, Robert
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CURRENT PILING DATE: 1932-06-09
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; TYDE. NO. 245
; TENGTH: 822
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 821
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1.3%; Score 23; DB 3; Length 821;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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US-09-328-475C-191/C
Sequence 191, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: ABtel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1691 AAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(821)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-249
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i_CCATION: (1)...(822)
/_CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-245
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NAME/KEY: misc_feature
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Matches 23; Conserva
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Caracial III, Eddie
APPLICANT: Caracial III, Eddie
APPLICANT: Ford Donna M.
APPLICANT: Ford Donna M.
APPLICANT: Ford Donna M.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
CURRENT FILLING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 255
LENGTH: 830
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82 AAGTACCTCGGCCGCGACCACGC 60
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; Sequence 255, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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US-09-328-475C-225
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US-09-328-475C-103/c
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                                                APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GRKES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GRKES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REPERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-43
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-102
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Best Local Similarity
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                                                                                                                                                                    APPLICANT: Ford, Doma M.
APPLICANT: Ford, Doma M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTHARE: PEASISEQ for Windows Version 3.0
SEQ ID NO 103
LENGTH: 1021
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APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1332.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 1024
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US-09-328-475C-51/C
iSequence 51, Application US/09328475C
iFatent No. 6476207
iFATENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
Sequence 103, Application US/09328475C Patent No. 6476207
GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie APPLICANT: Bndege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AAGTACCTCGGCCGCGACCACGC 79
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NAME/KEY: misc feature
LOCATION: (1)...(1021)
COTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.
Matches 23; Conservative
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Matches 23; Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Actal, John
APPLICANT: Actal, John
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Endegel, Robert
APPLICANT: Schlegel,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 78, Application US/09328475C

Fatent No. 6476207

GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy

APPLICANT: Carroll III, Eddie

APPLICANT: Endege, Wilson O.

APPLICANT: Endege, Wilson O.

APPLICANT: Endege, Wilson O.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Steinmann, Kathleen E.

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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                          0; Indels
                                                                                               DB 3;
0.61;
                                                                                         Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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LOCATION: (1)...(1024)
OTHER INFORMATION: n = A,T,C or G
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Matches 23; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 39
US-09-328-475C-77/c
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US-09-328-475C-78
US-09-328-475C-71
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III; Eddie
APPLICANT: Carroll III; Eddie
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III; Eddie
APPLICANT: Brdege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENEE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENEE AND GENE EXPRESSION PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT PELLIG DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 71
SEQ ID NO 71
LENGTH: 1024
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1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
                                            1691 AAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                    RESULT 37
US-09-328-475C-56/C
; Sequence 56, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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US-09-328-475C-71/C
Sequence 71, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-56
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OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
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ORGANISM: Homo Sapien
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; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
TYPE: DNA
; ORGANISM: Homo sapien
; FRATURE:
; LOCATION: (1) ... (2051)
; OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Myxococcus xanthus
US-09-902-540-866
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APPLICANT: Goldman, Barry S.
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Best Local Similarity
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US-09-902-540-8302
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US-09-902-540-866
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Ford, Doma M.
APPLICANT: Ford, Doma M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Redere EXPRESSION PRODUCTS THAT
ITLE OF INVENTION: AEB DIFFERENTIALLY REGULATED IN PROSTATE CANCER
ITLE OF INVENTION: ABE DIFFERENTIALLY REGULATED IN PROSTATE
CURRENT FILING DATE: 1999-06-09
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 93
LENGTH: NAME
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US-09-328-475C-334
US-09-328-475C-334

| Sequence 334, Application US/09328475C
| Patent No. 6476207
| GENERAL INFORMATION:
| APPLICANT: Zhang, Jimmy
| APPLICANT: Carroll III, Eddie
| APPLICANT: Endes, Wilson O. | APPLICANT: Endes, Wilson O. | APPLICANT: Schlegel, Robert
| APPLICANT: Schlegel, Robert
| APPLICANT: Schlegel, Robert
| APPLICANT: Schlegel, Robert
| TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
| TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER | TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER | TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER | TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER | TITLE OF INVENTION NUMBER: US/09/328,475C
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                                                                                                                                                                                                                           0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                         Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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; Sequence 93, Application US/09328475C
; Datent No. 6476201
; GENERAL INFORMATION:
                                                ) NAME/KEY: misc_feature

) LOCATION: (1)...(1024)

) OTHER INFORMATION: n = A,T,C or G

US-09-328-475C-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // LOCATION: (1)._.(1024)
// OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-93
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       ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Sequence 8302, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVERTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 05/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8302
LENGTH: 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Migrand, Moger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 866
LENGTH: 6339
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Query Match 1.3%; Score 23; DB 3; Length 2051; Best Local Similarity 100.0%; Pred. No. 0.61; Matches 23; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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  Score 23; DB 3; Length 6339;
Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Wumble, Krishanand D.
TITLE OF INVENTION: compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions For Their Use
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION WUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
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Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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                                                                                                             1190 GGACCTGCACCTGCCGGAGATGG 1212
                                                                                       666 GGACCTGGACCTGCCGGAGATGG 688
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GENERAL INFORMATION:
                                                                                                                                                                                                                                       ; Sequence 4, Application US/09188930A; Patent No. 6150502
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Matches 22; Conservative
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Matches 22; Conservative
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ORGANISM: Human
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ORGANISM: Mouse
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US-09-312-283C-4/c
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LENGTH: 311
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APPLICANT: Sun, Yongwing
APPLICANT: Sun, Yongwing
APPLICANT: Chen, Sei-Yu
APPLICANT: Lean, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Lean
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFRENCE: DEX-0241
CURRENT PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/242,998
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 277
SOFTWARE: Patentin version 3.1
SEQ ID NO 138
LENGTH: 352
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Stelimann, Kathleen E.
APPLICANT: Stelimann, Kathleen E.
TITLE OF INVENTION: GREEN DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: GREEN DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: QREEN DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 237
LENGTH: 483
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1.3%; Score 22; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches
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NAME/KEY: misc feature

LOCATION: (1)...(483)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-002-344A-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapien
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Sequence 200, Application US/09328475C
                Patent No. 6476207
GENERAL INFORMATION:
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Sequence 194, Application US/09328475C

Patent No. 6476207

GENERAL INPORMATION:

APPLICANT: Zhang, Jummy

APPLICANT: Astel, Jon H.

APPLICANT: Endege, Wilson O.

APPLICANT: Endege, Wilson O.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSTATE CANCER

TITLE REFERENCE: 1532.002/200130.4638

CURRENT APPLICATION NUMBER: 183(99/328,475C)

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 194

SEQ ID NO 194

LENGTH: 502
  MS-09-328-475C-222/C

WS-09-328-475C-222/C

Sequence 222, Application US/09328475C

Sequence 222, Application US/09328475C

GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GARE APPLICANT:
TITLE OF INVENTION: GENES AND GARE APPLICANT:
CURRENT FAPLING DATE: 199-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0

SENGTH 407
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Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches
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1.3%; Score 22; UBBest Local Similarity 100.0%; Pred. No. 1.9
Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo Sapien
US-09-328-475C-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-194
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Squence 8248, Application US/10131827

Squence 8248, Application US/10131827

Squence 8248, Application US/10131827

GENERAL INFORMATION:

APPLICANT: Woolgemuth, Jay

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

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APPLICANT: Woodward, Ro
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APPLICANT: Change, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Stelagel, Robert
APPLICANT: Stelagel, Robert
APPLICANT: Stelagel, Robert
APPLICANT: Stelagel, Robert
APPLICANT: Stelagel, Robert
APPLICANT: Stelagel, Robert
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APPLICANT: Stelagel, Robert
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.(
Matches 22; Conservative
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CORGANISM: Homo sapiens
US-10-131-827-8248
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ORGANISM: Homo Sapien
FEATURE:
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RESULT 51 US-09-328-475C-200/c

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1692 AGTACCTCGGCCGCGACCACGC 1713
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Patent No. 6476207
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                               122 AGTACCTCGGCCGCGACCACGC 101
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LOCATION: (1)...(771)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Garroll III, Eddie
APPLICANT: Endege, Wilson O.
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Matches 22; Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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US-09-328-475C-176/c
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US-09-328-475C-169
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APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 281
LENGTH: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhangy, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Garroll III, Eddie
APPLICANT: Bradege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSUCTS THAT
TITLE OF INVENTION: ARE DIPPERBRUIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 280
LENGTH: 751
LENGTH: 751
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US-09-328-475C-280/c
'S Sequence 280, Application US/09328475C
'Patent No. 647620'
'GENERAL INFORMATION:
US-09-328-475C-281/c
; Sequence 281, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-281
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-280
                                                                                                  APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
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ORGANISM: Homo Sapien
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Sequence 176, Application US/09328475C

Sequence 176, Application US/09328475C

Patent No. 64762D1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Bendey, Wilson O.
APPLICANT: Bord, Donna M.
APPLICANT: Schlegel, Wobert
APPLICANT: Schlegel, Robert

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
TITLE OF INVENTION ARE DIFFERENTIALLY REGULATED IN PROSTATE
TITLE REFERENCE: 1532.002/20013/0.463
CURRENT APPLICATION NUMBER: US/09/328, 475C
CURRENT PILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341

SEQ ID NO 176

LENGTH: 773

FURNITH 773

FURNITH 773
APPLICANT: Ford, Dona M. APPLICANT: Ford, John E. APPLICANT: Schlegell, Robert APPLICANT: Schlegell, Robert APPLICANT: Schlegell, Robert APPLICANT: Steinmann, Kathleen E. TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT TITLE OF INVENTION: ARE DIFPERENTIALLY REGULATED IN PROSTATE CANCER FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 169
LENGTH: 771
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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i.CCATION: (1)...(773)
CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-176
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US-09-328-475C-238
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US-09-328-475C-168/C

| Sequence 168, Application US/09328475C
| Patent No. 6476207
| GENERAL INFORMATION:
| APPLICANT: Zhang, Ulmmy
| APPLICANT: Astel, Jon H.
| APPLICANT: Endege, Wilson O.
| APPLICANT: Ford, Donna M.
| APPLICANT: Schlegel, Robert
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Bridge, Wilson O.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
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APPLICANT: Schlegel, Robert
APPLICA
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1.9;
DB 3; Length 773;
1.9;
                                                                                                                   0; Indels
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Query Match 1.3%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 57
US-09-328-475C-163/c
Sequence 163, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
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CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-163
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Sequence 238, Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy

APPLICANT: Abtel, Jon H.

APPLICANT: Badege, Wilson O.

APPLICANT: Bondahan, John E.

APPLICANT: Schlegel, Robert

APPLICANT: Steinmann, Kathleen E.

APPLICANT: Steinmann, Kathleen E.

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSTATE CANCER

TITLE OF INVENTION: 1999-06-09

CURRENT APPLICANT: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FASTESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Badege, Wilson O.
APPLICANT: Bodege, Wilson O.
APPLICANT: Mondan, John E.
APPLICANT: Mondan, John E.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENERE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
FILE REPERENCE: 1332.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NOWER: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SET IN O 119
TYPE: DNA
COGANISM: HOMO Sapien
                                                                                                                                                                                      Gaps
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                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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8-09-328-475C-119/c
; Sequence 119, Application US/09328475C
; Patent No. 6476207
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                                                                                                                                                                                                                                                                                             102 AGTACCTCGGCGCGACCACGC 81
; NAME/KEY: misc_feature
; LCCATION: (1)...(780)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-168
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NAME/KEY: misc_feature
LOCATION: (1)._.(811)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.
Matches 22; Conservative
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APPLICANT: Shangy Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Bridge, Wilson O.
APPLICANT: Bridge, Wilson O.
APPLICANT: Mondan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
ITILE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
ITILE OF INVENTION: GENES AND GENES EXPRESSION PRODUCTS THAT
ITILE OF INVENTION: GENES AND GENES EXPRESSION PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICANTION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE PARTSEQ for Windows Version 3.0
SEQ ID NO 104
LENGTH: 1017
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1.9;
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1.3%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 22; Conservative 0; Mismatches
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 195
LENGTH: 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 AGTACCTCGGCCGCGACCACGC 78
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; Sequence 57, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Homo Sapien
FRATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(848)
CTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-104
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Endege, Wilson O.
Ford, Donna M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
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APPLICANT:
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III; Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schiegel, Kobert
APPLICANT: Schiegel, Kobert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GREENE ENPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER
FILE REPERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NOS: 341
LENGTH: 822
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Sequence 195, Application US/09328475C

Sequence 195, Application Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Seque
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                                                                                                                                                                                                                                                                                                                                          Query Match 1.3%; Score 22; DB 3; Length 815; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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OTHER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: n = A,T,C or G
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1es 22; Conservative
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                                                                TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
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SEQ ID NO 238
LENGTH: 815
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US-09-328-475C-65/C

US-09-328-475C-65/C

Sequence 65. Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, John H.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, Varhlen E.
APPLICANT: Standarn, ARR DIFFERENTIALLY REGULATED IN PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: NUMBER OF SEQ ID NO 65
LENGTH: NUMBER OF SEQ ID NO 65
LENGTH: NUMBER OF SEQ ID NO 65
APPLICANT: Zhang, Jimmy
APPLICANT: Ascel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schiegel, Robert
APPLICANT: Schiegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSUCTS THAT
TITLE OF INVENTION: 1992-06-09
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 62
EMPORT: PastSEQ for Windows Version 3.0
SEQ ID NO 62
EMPORT: PAST OF SEQ ID ABORD SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE PAST OF SECON FOR THE
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1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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CCATION: (1)...(1024);
CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-62
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LCCATION: (1)...(1024)

CTHER INFORMATION: n = A,T,C or G

US-09-328-475C-65
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Best Local Similarity 100.C
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
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ORGANISM: Homo Sapien
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APPLICANT: Astel Jon H.
APPLICANT: Astel Jon H.
APPLICANT: Carroll III. Eddie
APPLICANT: Carroll III. Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Stelmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIPPERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT PILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 61
LENGTH: 1024
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APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 57
LENGTH: 1024
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US-09-328-475C-62/c
; Sequence 62, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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// Patent No. 6476207
// GENERAL INFORMATION:
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NAME/KEY: misc_feature

LOCATION: (1)...(1024)

OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-61
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Best Local Similarity 100.
Matches 22; Conservative
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ORGANISM: Homo Sapien
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US-09-328-475C-61
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APPLICANT: ABTEL, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Bridege, Wilson O.
APPLICANT: Schlegel, Robert
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APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, R
Sequence 73, Application US/09328475C

Sequence 73, Application US/09328475C

Fatent No. 647607

GENERAL INFORMATION

APPLICANT: Astel, Jon H.

APPLICANT: Carroll III, Eddie

APPLICANT: Carroll III, Eddie

APPLICANT: Ford, Donna M.

APPLICANT: Ford, Donna M.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE

CURRENT APPLICATION NUMBER: US/09/328,475C

CURRENT APPLICATION NUMBER: US/09/328,475C

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CURRENT APPLICATION NUMBER: US/09/328,475C

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CURRENT APPLICATION NUMBER: US/09/328,475C
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US-09-328-475C-75/c
; Sequence 75, Application US/09328475C
; Patent No. 6476207
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i_CCATION: (1)...(1024)
i_CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-73
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-75
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ORGANISM: Homo Sapien
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18 SEGURE 475C-79
18 SEGURE 60 5467207
18 SEGURE 60 79, APPLICATION 19 SEGURE 60 79, APPLICATION 19 SEGURE 60 79, APPLICATION 19 SEGURE 60 79, APPLICATION 19 SEGURE 60 79, APPLICANT 19 SEGURE 60 70 SEGURE 60 70 SEGURE 60 70 SEGURE 60 70 SEGURE 60 70 SEGURE 60 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SEGURE 70 SE
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Sequence 249, Application US/09312283C
; Sequence 249, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
; TITLE OF INVENTION: and Methods for Their Use
; TITLE OF INVENTION: 10101c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 249
...ENGTH: 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 249, Application US/09188930A
; Sequence 249, Application US/09188930A
; Sequence 249, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
    APPLICANT: Strachan, Lorna
    APPLICANT: Strachan, Lorna
    APPLICANT: Strachan, Matthew
    APPLICANT: Murison, James Greg
    TITLE OF INVENTION: Compositions Isolated From Skin Cells
    TITLE OF INVENTION: and Methods For Their Use
    TITLE REPERENCE: 11000.1011c1
    CURRENT APPLICATION NUMBER: US/09/188,930A
    CURRENT FILING DATE: 1998-11-09
    NUMBER: OF SEQ ID NOS: 348
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 249
    LENGTH: 11212
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indel8
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                                                                                                                                                                  Length 1024;
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Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches (
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-86
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nes 22, Conservative
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Best Local Similarity
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; ORGANISM: Human
US-09-188-930-249
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Sequence 86, Application US/09328475C

Sequence 86, Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:

APPLICANT: Astel, Jon H.

APPLICANT: Endeg, Wilson O.

APPLICANT: Endeg, Wilson O.

APPLICANT: Schlegel, Nobert

APPLICANT: Schlegel, Nobert

TILLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: Athleen E.

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TILLE REFERENCE: 1532.002/200130.463

CURRENT FILLING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 86

SEQ ID NO 86

LENGTH: AVENTION: ARE LENGTH AND OF SEQ ID NO 86

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LENGTH: AVENTION OF SEQ ID NOS: 341

LENGTH: AVENTION OF SEQ ID NOS: 341
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Zhang, Jinmwy
APPLICANT: Astel, Jon H.

APPLICANT: Carroll III; Eddie
APPLICANT: General Milson O.

APPLICANT: Ford, Donna M.

APPLICANT: Monehan, John E.

APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Rathleen E.

TITLE OF INVENTION: GENER AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
FILE REFERENCE: 1532.002/200130.463

CURRENT APPLICATION NUMBER: US/09/328,475C

CURRENT APPLICATION NUMBER: US/09/328,475C

CURRENT APPLICATION NUMBER: 1399-06-09

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 82
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                            1.3%; Score 22; DB 3; Length 1024; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indels
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                                                                                                                                           1692 AGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                          110 AGTACCTCGGCCGCGACCACGC 89
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18-09-328-475C-82/c
Sequence 82, Application US/09328475C
Patent No. 6476207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LUCCATION: (1)._.(1024); OTHER INFORMATION: n = A,T,C or GUS-09-328-475C-82
                                                                                  22; Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
                            Query Match
Best Local Similarity
                                                                                  Matches
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Sequence 319, Application US/09389681A
| Sequence 319, Application US/09389681A
| Patent No. 6518237
| GENERAL INFORMATION:
| APPLICANT: Yuqui, Jiang
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
| TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
| TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
| TITLE OF INVENTION: UNDERS: US/09/389,681A
| CURRENT FILING DATE: 1999-09-02
| NUMBER OF SEQ ID NOS: 463
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 319
| LENGTH: 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.2%; Score 21; DB 3; Best Local Similarity 100.0%; Pred. No. 5.7; Matches 21; Conservative 0; Mismatches
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1.2%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 5.7
Matches 21; Conservative 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Jiang Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1693 GTACCTCGGCCGCGACCACGC 1713
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ORGANISM: Homo sapiens
FEATURE:
LOCATION: (1)...(241)
OTHER INFORMATION: n = A,T,C or G
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| LOCATION: (1)...(241)

| CTHER INFORMATION: n = A,T,C or G

US-09-389-681-319
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ORGANISM: Homo sapiens
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US-09-389-681-319
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APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANTON: WITHOUS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PARENTL VERSION 3.1
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Moc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE REPERENCE: So6612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT PILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
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100.0%; Pred. No. 5.7;
ive 0; Mismatches 0; Indels
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1.2%; Score 21; DB 3; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels
  0; Indels
  0; Mismatches
                                                    1692 AGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                      ; Sequence 8652, Application US/10131827; Patent No. 6905827; GENERAL INFORMATION: APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8632, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.
Matches 21; Conservative
22; Conservative
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US-10-131-827-8632
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US-10-131-827-8652
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US-10-131-827-8632
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SEQ ID NO 8632
LENGTH: 240
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Matches
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1693 GTACCTCGGCCGCGACCACGC 1713

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GENERAL INFORMATION:

APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.

APPLICANT: Dillon, Davin C.

APPLICANT: Wicham, Jennifer L.

APPLICANT: William T.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Henderson, Robert A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

TITLE OF SEQ ID 121.470C9

CURRENT APPLICATION NUMBER: US/09/834,759

CURRENT FILING DATE: 2001-04-13

SOFTHARE: FESTSEQ for Windows Version 3.0

SEQ ID NO 319

LENGTH: 241
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Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: My, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C6
CURRENT APPLICATION NUMBER: US/09/590,751A
CURRENT FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 479
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 241
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APPLICANT: Yuqui, Jiang
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                                                                                                                               Sequence 319, Application US/09834759
Patent No. 6680197
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  208 GTACCTCGGCCGCGACCACGC 228
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NAME/KEY: misc_feature
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LOCATION: (1)...(241)
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ORGANISM: Homo sapiens
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                                                                               RESULT 82
US-09-834-759-319
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Mitchan Compositions for the treatment and TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND TITLE OF INVENTION: LAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.470C4
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 474
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 241
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Sequence 319, Application US/09604287A

GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Mu, Jiangchun J.
APPLICANT: Wu, Jiangchun J.
APPLICANT: Wu, Jiangchun J.
APPLICANT: William I.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: DINVENTION: COMPOSITIONS OF BREAST CANCER
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C7

CURRENT APPLICATION NUMBER: US/09/604,287A

CURRENT FILING DATE: 2000-06-22
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100.0%; Pred. No. 5.7;
tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 241
                                                                                                                      Sequence 319, Application US/09433826B
Patent No. 6579973
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqui
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208 GTACCTCGGCCGCGACCACGC 228
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NAME/KEY: misc_feature
LOCATION: (1)...(241)
OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-319
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Matches 21; Conservative
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ORGANISM: Homo sapiens
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                                                                                                        US-09-433-826B-319
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US-09-604-287A-319
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APPLICANT: Houghton, Raymond L.

APPLICANT: Bleath, Paul R.

APPLICANT: Sleath, Paul R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210.21.470C11

CURRENT APPLICATION NUMBER: 120.20.20.3

NUMBER OF SEQ ID NOS: 627

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 319
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APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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100.0%; Pred. No. 5.7;
tive 0; Mismatches 0; Indels
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                                                                        RESULT 86
US-10-076-622-319
'Sequence 319, Application US/10076622
'Patent No. 6958361
  208 GTACCTCGGCCGCGACCACGC 228
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Patent No. 6329505
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
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NAME/KEY: misc feature
LOCATION: 24, \overline{3}6, 39
OTHER INFORMATION: n = A,T,C or G
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Reed, Steven G.
Kalos, Michael
Fanger, Gary
Retter, Mark
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Best Local Similarity 100.
Matches 21; Conservative
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) ORGANISM: Homo sapien
US-09-439-313-293
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APPLICANT:
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Sequence 319, Application US/09551621A

Sequence 319, Application US/09551621A

Sequence 319, Application US/09551621A

GENERAL INFORMATION:

APPLICANT: Yulion, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: UNMBER: 105/09/551,621A

CURRENT APPLICATION NUMBER: 105/09/551,621A

CURRENT FILING DATE: 2000-04-17

NUMBER OF SEQ ID NOS: 479

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 319

LENGTH: 241

TURE OF INVENTION: WINDOWS VERSION 3.0
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Davin C.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C5
CURRENT APPLICATION NUMBER: US/09/551,621
CURRENT FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 479
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 241
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                                                                                                                                              Sequence 319, Application US/09551621
Patent No. 6825175
GENERAL INFORMATION:
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                     208 GTACCTCGGCCGCGACCACGC 228
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; OTHER INFORMATION: n = A,T,C or G
US-09-551-621-319
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LCCATION: (1)...(241)

CTHER INFORMATION: n = A,T,C or G

US-09-551-621A-319
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US-09-551-621-319
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TYPE: DNA

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Gaps

TYPE: DNA

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER PILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
                                                                                                                                                                                                                                                                                                                                                     Query Match 1.2%; Score 21; DB 3; Length 301; Best Local Similarity 100.0%; Pred. No. 5.7; Matches 21; Conservative 0; Mismatches 0; Indels
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                           CURRENT APPLICATION NUMBER: US/09/159,812A CURRENT FILING DATE: 1998-09-23 NUMBER OF SEQ ID NOS: 306 SEQ TO NO 233 EQ ID NO 233 LENGTH: 301
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Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Patent No. 6620922
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Skeiky, Yasir A.W.
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Vedvick, Thomas S.
Carter, Darrick
FILE REFERENCE: 210121.428C5
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Best Local Similarity 100.0
Matches 21, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
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                                                                                                                                                                                                                           TYPE: DNA; ORGANISM: Homo sapien
US-09-159-812-293
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CORGANISM: Homo sapien
US-09-636-215-293
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APPLICANT: Xu, Jian
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                  JOURNAL OF STATE OF THE REFERENCE: 1999-07-35.

JOURNAL OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE O
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Sequence 293, Application US/09232149A

FAPELORY: No. 6465610:
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jounifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 21012.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT APPLICATION NUMBER: US/09/232,149A

NUMBER OF SEQ ID NOS: 338

SOFTWARER: FastSEQ for Windows Version 3.0
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APPLICANT: Xu, Jiangchun
APPLICANT: Xi, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
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100.0%; Pred. No. 5.7;
vative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 21; Conservative
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; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-293
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ORGANISM: Homo sapien
US-09-352-616A-293
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US-09-159-812-293
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LENGTH: 301
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APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSEQ for Windowe TENGTH: 301
TYPE: No. 293
LENGTH: 301
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APPLICANT: Kang, Aiun
APPLICANT: Resiry, Yasir A.W.
APPLICANT: Replex, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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100.0%; Pred. No. 5.7;
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Best Local Similarity 100.0%; Pred. No. 5.7;
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SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6800746
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Susan L.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Matches 21; Conservative
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ORGANISM: Homo sapien
US-09-759-143-293
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CORGANISM: Homo sapien
US-09-679-426-293
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US-09-759-143-293
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helpler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
FILE REPERROE: 21012.427021
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SEGTWARE: PASISEQ for Windows Version 3.0
SECTRARE: PASISEQ for Windows Version 3.0
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; Sequence 293, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; TILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
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                Henderson, Robert A.
Kalos, Michael D.
                                                                                                   Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Best Local Similarity 100.
Matches 21; Conservative
                                                              Fanger, Gary R.
Retter, Marc W.
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; ORGANISM: Homo sapien
US-09-685-166A-293
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CORGANISM: Homo sapien
US-09-688-489-293
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Matches 21; Conserva
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US-09-688-489-293
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US-09-679-426-293
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 21012.427C19
CURRENT APPLICATION NUMBER: US/09/657,279
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
AITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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100.0%; Pred. No. 5.7;
tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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CURRENT FILING DATE: 2001-12-10
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Heppler, William T.
Henderson, Robert A.
Hural, John
MCMSill, Particia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Patent No. 6943236
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
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Best Local Similarity 100.0
Matches 21; Conservative
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Best Local Similarity 100.
Matches 21, Conservative
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COGGANISM: Homo sapiens
US-10-012-896-293
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                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapien
US-09-657-279-293
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: Fastern f
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Pred. No. 5.7;
0; Mismatches 0; Indels
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     Mismatches
                                       1693 GTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                      US-09-651-236-293
; Sequence 293, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
                                                                       232 GTACCTCGGCCGCGACCACGC 252
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Best Local Similarity 100.0%; P.
Matches 21; Conservative 0;
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Kalos, Michael D.
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Jiang, Yuqui
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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Retter, Marc W.
Stolk, John A.
     21; Conservative
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ORGANISM: Homo sapien
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LENGTH: 301
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APPLICANT: LY, NGCC
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT PILING DATE: 2002-09-06
PRIOR PILING DATE: 2001-09-06
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin Version 3.1
SEQ ID NO 8546
LENGTH: 311
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Patent No. 6150502

GERERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Sleeman, Matthew

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: 1900.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FRALSEQ for Windows Version 3.0

SEQ ID NO 71

LENGTH: 378

TYPE: DNA

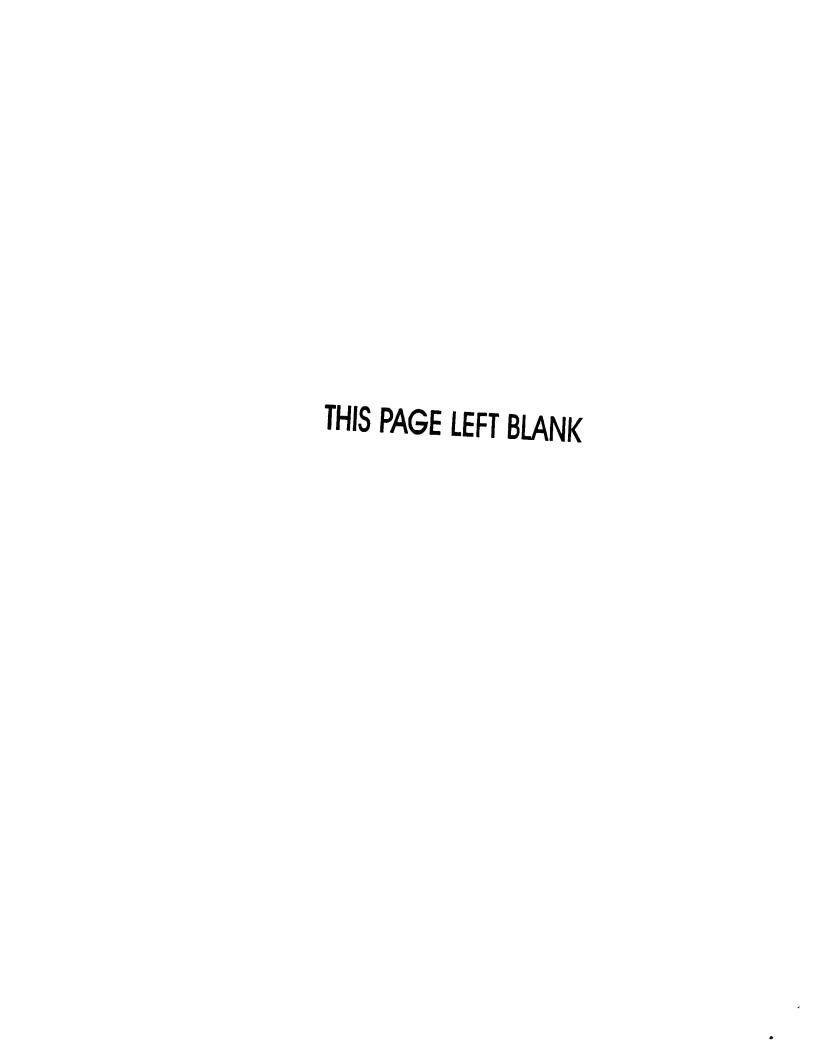
CREANISM: Human

US-09-188-930-71
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Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels
                                              Sequence 8546, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Pry, Kirk
APPLICANT: Pry, Kirk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8546
RESULT 99
US-10-131-827-8546
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US-09-188-930-71/c
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111	RESULT 2 US-10-104-047-799 iSequence 799, Application US/10104047 ; Publication No. US20030236392A1 ; GENERAL INFORMATION:     APPLICANT: HELIX RESEARCH INSTITUTE     TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA ; FILE REFERENCE: HI-A0105 ; CURRENT FILING DATE: 2002-03-25 ; CURRENT FILING DATE:     PRIOR FILING DATE:     NUMBER: OF SEQ ID NOS: 4096 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 799     LENGTH: 1785 ; TYPE: DNA     ORGANIEM: Homo sapiens US-10-104-047-799	Ouery Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Qy 1 ATGCCCGCCCTGGACACCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACGTGGGAG 60
ATGCCCGCCCTGGACACCCCGCCCAACATCTGGGCCTCCACGTTGGGACCGTGGGAG	661 GAGTCGGACCTGGACCGGAGATGGGCAGTCGACCCATGTCGAGCCGAGAATTGAT 720  [	961 ACTCGGGCTGCTCCCAACCGCTGCTCCTGACAGTGGCCATGAGACCATGGTGGGC 1020

Db   921 CATGAGTCGGACCTGCCGGAGATGGGCAGTGCTCCATGTCGAGCCGAGAATT   980	; Sequence 117, Application US/0998920; Batent No. US20020172957A1; GENERAL INFORMATION; APPLICANT: Macina, Roberto; APPLICANT: Recipon, Herve APPLICANT: Recipon, Herve APPLICANT: Chen, Sei-Yu APPLICANT: Chen, Sei-Yu APPLICANT: Liu, Chenghua; TITLE OF INVENTION: Compositions and Methods; FILE REFERENCE: DEX. O291; CURRENT APPLICATION NUMBER: US/09/989,920; CURRENT FILING DATE: 2000-11-21; PRIOR PRILING DATE: 2000-11-22; NUMBER OF SEQ ID NOS: 284; SOFTWARE: PRECENT NOWER: 2000-11-22; NUMBER OF SEQ ID NOS: 284; SOFTWARE: Patentin version 3.1; LENGTH: 1977; TYPE: DNA; COGANISM: Homo sapien	Relating to Lung Specific Genes and Prot
OY 1017 GGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTCTCCCAGGAGACGACTGCAGA 1076	Query Match 57.4%; Score 983; DB Best Local Similarity 99.9%; Pred. No. 0; Matches 1103; Conservative 0; Mismatches	B 3; Length 1977; 0; Indels 1; Gaps 1;
QY         1077 TGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAAGGTACCCAGCAAGCCATGACTC 1136           Db         1341 TGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCCAGGTACCCAGCAAGCCATGACTC 1400	Qy 598 CACAGCCTGCCCAGCACTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTC	CGTGGCTCCGAGGACTACTATTCTTTC 657 
Oy         1137 ATCCTTCCAGGGCACCGACCAGACTCGTCGGGGGCACCCCTTGCTCCAGGTGTACTGCTA         1196           I	Qy 658 CATGAGTCGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATT	AGTGGCTCCATGTCGAGCCGAGAAATT 717 
QY         1197 ACCCCTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAG 1256           DD	Qy 718 GATGTGCTCATCTTCAAGAAGCTGACAGA-GCTGTTCAGCGTACACCAGATCGATGAGCT Dy 981 GATGTGCTCATCTTCAAGAAGCTGACAGAGGCTGTTCAGCGTACACAGATCGATGAGCT	GTTCAGCGTACACCAGATCGATGAGCT 776 
Qy         1257         AGGGGACCAGGAACCCCTGTGGGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTC         1316           Db         1521         AGGGGAACCAGGAACCCTGTGGGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTC         1580	Qy 777 GGCCAAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTAT	GAAGACCAGTAAGATCTCGGACCTTAT 836 
OY 1317 CTCCTGCCTTGGCTGGCTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTA 1376	Qy 837 CAGCAGCATACACGAGGACTACCACGATGAGCAGGATGCTGAGGGCCGCCTGGTACG	GCAGGATGCTGAGGCCGCCTGGTACG 896 
143(	OY 897 CGGCATCATTCGCATTAGTACCCGAAAGACCGTGCTCGCCCACAGACCTCGGAGGGTCG	TGCTCGCCCACAGACCTCGGAGGTCG 956 
OY 1437 GECTTCAGGEGCCCTGAICGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1496 	QY         957 ITCAACTGGGGTGCTCCCAACCGGTGCTGCCCTGACAGTGGCCATGGT           Db         1221 ITCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGT	CCCTGACAGTGGCCATGAGACCATGGT 1016 
OY 1497 CCTGACTCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTCGGG 1556	Qy 1017 GGGCTCAGGTCTCAGCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGACTGCAGA	GCAGATCTCCCAGGAGACGACTGCAGA 1076 
OY         1557         TAAITCAACAGITAAAAGAAGCITAICITAAAAGTAITGIAITGGGGGGGGGG	Qy 1077 TGCCATGGCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGGAAGCCATGACTC DY TGCCATGCAAGCCATGACTC DY 1341 TGCCATGCCCGGAAGCTGAGGCCTTATGGAGCTCAGGGTACCCAGGAAGCCATGACTC	TCCAGGGTACCCAGCAAGCCATGACTC 1136 
Qy 1617 CACTCTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTATCTTAACA 1676	Qy         1137 AFCCTTCCAGGGCACCGACACACAGAGACACCCTTGCTCCAGGTGTACTGCTA           1401 AFCCTTCCAGGGCACCGACAGACTCGTCGGGGGCACCCTTGCTCGGGTGTACTGCTA	GGCACCCTTGCTCCAGGTGTACTGCTA 1196 
Qy         1677 TGACCACAGTTTGTAAGTACCTCG 1700           Db         1941 TGACCACAGTTTGTAAGTACCTCG 1964	Qy         1197         ACCCCTGCCAGGCCCAGGCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAG           Db         1461         ACCCCTGCCAGGCCCAGCTGCCACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAG	GGGAGAAGCATGGCCTACAGAATGAAG 1256 
	Oy 1257 AGGGGACCAGGAACCCCTGTGGGGAGAGCTTAGACCTGAAGCAGTGCCCACTCTGGCTC	GACCTGAAGGAGTGCCACTCTGGCTC 1316
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APPLICANT: Macina, Roberto
APPLICANT: Racina, Roberto
APPLICANT: Racina, Herve
APPLICANT: Recipon, Herve
APPLICANT: Pluta, Jason
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANTON: Compositions and Methods Relating to Breast Specific Genes and Profurery APPLICATION NUMBER: US/09/989,890
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,509
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LIENGTH: 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1562
1430 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGG 1489
                                                                             1490 AGTGAACCCTGACTCCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTC 1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1323 CCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTC 1382
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                                                                                                    301 AGTGAACCCTGACTCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAAGGAGTTAGGCATTACCTTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 GCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 ACCAGGAACCCCTGTGGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 CCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTC
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                                                                                                                                                             1550 CCTGGGGTAATTCAACAGTTAAAAG 1574
                                                                                                                                                                                  361 CCTGGGGTAATTCAACAGTTAAAAG 385
                                                                                                                                                                                                                                                                                                 ; Sequence 104, Application US/09989890; Publication No. US20040166105A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AACAGTTAAAAGAAGCTT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-890-104
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US-09-989-890-104
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; Sequence 55, Application US/0998920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sel-Yu
; APPLICANT: Chen, Sel-Yu
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; TLE OF INVENTION COMPOSITIONS of 11-21
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR PILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
LUNGTH: 385
                       1581 CTCCTGCCTTGGCTGACTGGATCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTA 1640
                                                                                                  1437 GTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1496
                                                                                                                                                                                  1557 TAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATTGGGGGGGTGGGCAGGGCC 1616
                                                                                                                                                                                                                                                                                                                                               1617 CACTCTATGTTATGTTAAGGAGTTGGTTCTTGGCTGATGTTCTGTATCTTAACA 1676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CTGGCTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1677 TGACCACAGITIGIAAGIACCICG 1700
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; ORGANISM: Homo sapien
US-09-989-920-55
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US-09-989-920-55
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985 GCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTG 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 ACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTAT 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 GATGAGCAGGATGCTGAGGGCCCCTGGTACGCGCCATCATTCGCATTAGTACCCGAAAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 AGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          865 GATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAG 924
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                                        PRIOR FLILNG DATE: 1997-12-23
PRIOR PELING DATE: 1997-12-23
PRIOR PELING DATE: 1997-12-23
PRIOR PLING DATE: 1997-10-23
PRIOR PLING DATE: 1998-04-03
PRIOR PLING DATE: 1998-04-03
PRIOR PLING DATE: 1999-10-21
PRIOR PLING DATE: 1999-10-21
PRIOR PLING DATE: 1999-10-24
PRIOR PLING DATE: 1999-01-28
PRIOR PLING DATE: 1999-01-28
PRIOR PLING DATE: 1999-01-28
PRIOR PLING DATE: 1999-01-28
PRIOR PLING DATE: 1999-01-24
PRIOR PLING DATE: 1999-01-24
PRIOR PLING DATE: 1999-01-24
PRIOR PLING DATE: 1999-01-34
PRIOR PLING DATE: 1999-01-31
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PRIOR PLING DATE: 1998-01-31
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Publication No. US20050227917A1

GENERAL INFORMATION:

APPLICAT: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REFERENCE: 2300-2130

CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT FILING DATE: 2004-02-12

PRIOR FILING DATE: 2002-02-15

FRIOR FILING DATE: 2002-02-15
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US-10-779-543-10096
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LOCATION: 355
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Sequence 123, Application US/10074475

Publication No. US200300928981

SERNEAL INPORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Macina, Roberto
APPLICANT: Rerigon, Herve
APPLICANT: Karra, Kalpana
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghing
APPLICANT: Liu, Chenghing
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REPERENCE: DEX-0313
CURRENT APPLICATION NUMBER: 100/074,475
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR APPLICATION NUMBER: 60/268,292
MANDED OF COLOUR NUMBER: 1001-02-13
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Sequence 10096, Application US/10779543

PUBLICATION NO. US20050227917A1

GENERAL INFORMATION:
TITLE OF INVERMION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVERTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-2130

CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT PELING DATE: 2004-02-12

PRIOR FILING DATE: 2002-02-15
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100.0%; Pred. No. 1.4e-190;
iive 0; Mismatches 0;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 123
LENGTH: 386
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Matches 378; Conservative
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ORGANISM: Homo sapien
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1065 GACGACTGCAGGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGC 1124
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                                                      PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/068,755
PRIOR PILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR PILING DATE: 1998-01-021
PRIOR PILING DATE: 1999-01-021
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
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PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1998-01-24
PRIOR PILING DATE: 1998-01-24
PRIOR PILING DATE: 1998-02-31
PRIOR PILING DATE: 1998-03-31
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100.0%; Pred. No. 6.1e-149;
tive 0; Mismatches 0; Indels
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Innis, Michael A.
Garcia, Pablo bominiquez
Sudduth-Klinger, Julie
Reinhard, Christoph
Giese, Klause
Randazzo, Filippo
Kemnedy, Giulia C.
Pot, David
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Sequence 34, Application US/10076555

Publication No. US20030065156A1

GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
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Dickson, Mark
Drmanac, Snezana
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Lamson, George
Drmanac, Radoje
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Best Local Similarity 100.0
Matches 300; Conservative
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ORGANISM: Homo sapiens
US-10-779-543-1705
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APPLICANT:
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PRIOR APPLICATION NUMBER: 09/217,471
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-12-21
PRIOR PILING DATE: 1998-12-21
PRIOR PAPLICATION NUMBER: 60/068,755
PRIOR PILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/105,234
PRIOR PILING DATE: 1998-10-21
PRIOR PILING DATE: 1998-10-21
PRIOR PILING DATE: 1999-10-21
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1998-02-24
PRIOR PELING DATE: 1998-02-24
PRIOR PILING DATE: 1998-02-24
PRIOR PILING DATE: 1998-02-24
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PRIOR PILING DATE: 1998-03-31
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Publication No. US20050227917A1
GENERAL INFORMATION:
APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-23130
CURRENT APPLICATION NUMBER: US/10/779,543
CURRENT FILING DATE: 2004-02-12
PRIOR FILING DATE: 2002-02-15
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OTHER INFORMATION: n = A,T,C or G
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US-10-779-543-1705
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Sequence 124, Application US/10074475

Sequence 124, Application US/10074475

Publication No. US20030092898A1

GENERAL INFORMATION:

APPLICANT: Salceda, Susana

APPLICANT: Macina, Roberto

APPLICANT: Karra, Kalpana

APPLICANT: Cafferkey, Robert

APPLICANT: Liu, Youngming

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific

TITLE OF INVENTION: Compositions and Proteins

TITLE REPERENCE: DEX-0313

CURRENT FILING DATE: 2002-02-13

CURRENT FILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 295

SOFTWARE: PatentIn version 3.1

SEQ ID NO 124

LENGTH: 654
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PRIOR APPLICATION NUMBER: 60/105,234
PRIOR FILING DATE: 1999-10-21
PRIOR PILING DATE: 1999-10-21
PRIOR PLING DATE: 1990-10-6
PRIOR PLING DATE: 1990-10-8
PRIOR PLING DATE: 1990-10-8
PRIOR PLING DATE: 1990-01-28
PRIOR PLING DATE: 1990-01-28
PRIOR PLING DATE: 1990-01-28
PRIOR PLING DATE: 1990-01-28
PRIOR PLING DATE: 1990-02-4
PRIOR PLING DATE: 1990-02-4
PRIOR PLING DATE: 1990-02-4
PRIOR PLING DATE: 1990-02-4
PRIOR PLING DATE: 1990-02-4
PRIOR PLING DATE: 1990-02-31
PRIOR PLING DATE: 1990-02-31
SROWINGER OF SEQ ID NOS: 23767
SOFTWARE PRESEQ for Windows Version 4.0
SEQ ID NO 34
IENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     800 TGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACC
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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CORGANISM: Homo sapien
US-10-074-475-124
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; Publication No. US20050227917A1
; GENERAL INFORMATION:
    APPLICANT: Williams et al
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REPRENCE: 2300-21302
; CURRENT APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR PILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-23
; PRIOR FILING DATE: 1998-12-23
; PRIOR FILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 TGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACC
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Pred. No. 1e-121;
0; Mismatches 1; Indels
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Best Local Similarity 99.7
Matches 299; Conservative
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CORGANISM: Homo sapiens
US-10-076-555-34
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Sequence 669570, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPRENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 699570
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PRIOR FILING DATE: 1997-12-23
PRIOR PELICATION NUMBER: 60/068,755
PRIOR PELICATION NUMBER: 60/080,664
PRIOR FILING DATE: 1998-04-03
PRIOR PELICATION NUMBER: 60/105,234
PRIOR FILING DATE: 1998-10-21
PRIOR PELICATION NUMBER: 00/105,234
PRIOR PELICATION NUMBER: 00/0297,648
PRIOR PELING DATE: 1998-10-28
PRIOR PELING DATE: 1998-01-28
PRIOR PELICATION NUMBER: 60/072,910
PRIOR PELICATION NUMBER: 60/072,910
PRIOR PELICATION NUMBER: 60/072,910
PRIOR PELICATION NUMBER: 60/080,114
PRIOR PELICATION NUMBER: 60/080,114
PRIOR PELICATION NUMBER: 60/080,114
PRIOR PELICATION NUMBER: 60/080,114
PRIOR PELICATION NUMBER: 60/080,114
PRIOR PELICATION NUMBER: 60/080,114
PRIOR PELICATION NUMBER: 1998-03-31
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: 0F SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5731
LENGTH: 728
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
| LOCATION: 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 20,
| LOCATION: 2, 23, 24, 25, 28, 29, 30, 36, 41, 85, 89, 97, 106, 108,
| LOCATION: 115, 134, 139, 177, 185, 207, 232, 275, 283, 303, 320, 327,
| LOCATION: 356, 414, 451, 469, 551, 566, 582, 588, 591, 605, 631, 656, OTHER INFORMATION: n = A,T,C or G
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: 661, 681, 687, 689, 702, 706, 710, 711, 713, 722
| UCCATION: 661, 681, 681, 687, 689, 702, 706, 710, 711, 713, 722
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Factor 10. US20020172957A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Recipon, Herve

APPLICANT: Chen, Sei-Yu

APPLICANT: Chen, Sei-Yu

APPLICANT: Liu, Chenghuia

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot

FILE REFERENCE: DEX. Voognaming

APPLICANT: Liu, Chenghuia

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot

CURRENT PLING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-22

NUMBER OF SEQ ID NOS: 284

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1575 AAGCTTATCTTAAATGTATTGTATTGGGGGGGGGGCGCAGGCCCACTCTATGTTATGTTAA 1634
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                                                                                                                                             89 ATGATAAACCACCTCAGCCCCCACCAAGCCGCCGCACCGGTAGACCAGGACCCCAAGGACC 148
                                                                                                                                                                                                                                                                           61 CTGGCCACCATGGGCCAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTG 120
                                                                                                                                                                                                                                                                                                                                                                                                 209 AGTCCCCCACCTGCTGCCTGCTCTGGCGACCCTGGGTGTGGGGAGTGGTGCCGGGCTGCCT 268
                                                                                                                                                                                                         1 ATGATAAACCACCTCAGCCCCCACCAAGCCGCGCACCCGTAGACCAGACCCCAAGGACC 60
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Publication No. US20050227917A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REFERENCE: 2300-2310-2310-2313

CURRENT FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: 10/076,555

PRIOR APPLICATION NUMBER: 09/217,471
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                   Length 654;
                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 TCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 rerecricecececiecesearrecerecaecereresae 222
             Query Match 13.0%; Score 222; DB 5; Le Best Local Similarity 100.0%; Pred. No. 2.5e-107; Matches 222; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-989-920-116/c
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US-10-779-543-5731
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LENGTH: 120
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Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: 10DENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE REPRESENCE: MRI-007BGN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL LINGUART: Lee, John
APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: US 60/201,124
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-22
PRIOR PLILING DATE: 2000-07-22
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
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Publication No. US20030165831A1
GENERAL INFORMATION:
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37484
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ORGANISM: Homo sapiens
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US-10-357-930-7524/c
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Sequence 4813, Application US/10131827

Publication No. US20040009479A1

GENERAL INFORMATION:

APPLICANT: Woldgemuth, Jay

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: Ly, NGoc

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFERENCE: 50661200120

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFERENCE: 50661200120

CURRENT APPLICATION NUMBER: US 10/006,290

PRIOR APPLICATION NUMBER: US 10/006,290

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 9090

SEQ ID NOS: 9090

SEQ ID NOS: 9090

SEQ ID NOS: 9090
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Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Endege, Wilson

APPLICANT: Endege, Wilson

TITLE OF INVENTION: IDENTIFICATIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: IDENTIFICATION WHERE: US/10/357,930

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT APPLICATION NUMBER: US/10/357,930

PRIOR FILING DATE: 2000-02-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR PLING DATE: 2000-05-05

PRIOR PLING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

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    1 GATGTTAAGCTCAAAGGCATCCCTG 25
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LOCATION: (1)...(224)
OTHER INFORMATION: n = A, C, T or G
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ORGANISM: Homo sapiens
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US-10-357-930-37484/c
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RESULT 22
US-09-814-353-11387
US-09-814-353-11387
Sequence 11387, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lillia Usemela
APPLICANT: Lillia James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: USCOP. 12.01
FILE REPRERICE: MINIORIES: USCOP. 03-21
CURRENT FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: US 60/191, 031
PRIOR FILING DATE: 2000-05-25
PRIOR PELICATION NUMBER: US 60/211, 940
PRIOR PELICATION NUMBER: US 60/216, 820
PRIOR PELICATION NUMBER: US 60/216, 820
PRIOR PELING DATE: 2000-07-05
PRIOR PELING DATE: 2000-07-05
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-05
PRIOR PELING DATE: 2000-07-25
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PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELICATION NUMBER: US 60/257,672
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
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Publication No. US20030073144A1

GENERAL INFORMATION:

APPLICANT: Benson, Darin R.

APPLICANT: Lodes, Michael D.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Jang, Yugiu

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF PANCREATIC CANCER

FILE REPRENCE: 210121.566

CURRENT PALLICATION NUMBER: US/10/060,036

CURRENT PLING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4393
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100.0%; Pred. No. 0.039;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.04;
tive 0; Mismatches 0; Indels
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            280 GTAAGTACCTCGGCCGCGACCACGC 304
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Best Local Similarity 100.4
Matches 25; Conservative
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US-10-060-036-4393
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APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERBENCE: MI-066B
CURRENT PILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-25
PRIOR PAPLICATION NUMBER: US 60/207,124
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
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Pred. No. 0.04;
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR PELING DATE: 2000-02-17
PRIOR PELING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PRESEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 7524
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LOCATION: 123, 131, 149, 152, 166, 201, 284
OTHER INFORMATION: n = A,T,C or G
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US-09-814-353-5095
Sequence 5095, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Let John
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US-09-814-353-5095
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ORGANISM: Homo sapiens
FRATURE:
I_CCATION: 1, 3, 4, 5, 14, 18, 19, 20, 22, 26, 28, 29, 35, 36, 42, 46, 10CATION: 1, 3, 4, 5, 14, 18, 19, 20, 22, 26, 28, 29, 35, 36, 42, 46, 10CATION: 93, 96, 99, 102, 103, 107, 115, 116, 121, 124, 127, 146, 10CCATION: 169, 382, 433, 437, 465, 473, 480, 498, 517, 539, 541, 572
OTHER INFORMATION: n = A,T,C or G
FRATURE:
I_CCATION: 377, 591, 610, 627, 628, 657, 664, 672, 709, 712, 720, 726, 10CATION: 377, 539, 541, 572, 783, 784, 786, 772, 783, 789, 790, 797, 813, 814, 10CCATION: 915, 830, 835, 837, 846, 868, 873, 877, 896, 993, 921, 610, 627, 628, 657, 958, 974, 980, 985, 986
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 991, 996, 997, 999, 1001, 1002, 1008, 1010, 1015, 1018, 1019,
LOCATION: 1025, 1029, 1031, 1039, 1040, 1046, 1048, 1054, 1055, 1059,
LOCATION: 1060, 1063, 1067, 1068, 1069, 1070, 1072, 1075, 1079,
LOCATION: 1085, 1091, 1094, 1097, 1100, 1102, 1105, 1107, 1116
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                               Gaps
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| NAME/KR: misc_feature
| LOCATION: 1126, 1128, 1137, 1138, 1140, 1141, 1144, 1148, 1151,
| LOCATION: 1156, 1165, 1166, 1173, 1176, 1189, 1188, 1193, 1194, 1195,
| LOCATION: 1199, 1201, 1209, 1212, 1215, 1216, 1220, 1221, 1222, 1223,
| LOCATION: 1224, 1230, 1231, 1239, 1240, 1243, 1244, 1245, 1252
| UCHER INPORMATION: n = A,T,C or G
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                                                                                                                  DB 6; Length 810; 0.038;
                                                                                                                                                                                               0; Indels
                                                                                                              Query Match
1.5%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 25; Conservative 0; Mismatches
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; ORGANISM: Homo sapien
US-10-074-511-10
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| Sequence 10, Application US/10074511
| Publication No. US20030176672A1
| GENERAL INPORMATION:
| APPLICANT: Salceda, Susana
| APPLICANT: Racina, Roberto
| APPLICANT: Recipon, Herve
| APPLICANT: Recipon, Herve
| APPLICANT: Recipon, Herve
| APPLICANT: Recipon, Herve
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Yongming
| TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
| FILE REPERENCE: DEX. 2010/074,511
| CURRENT APPLICATION NUMBER: US/10/074,511
| CURRENT FILING DATE: 2001-02-13
| NUMBER OF SEQ ID NOS: 110
| SOFTWARE: Patentin version 3.1
| SOFTWARE: Patentin version 3.1
| SOFTWARE: Patentin Version 3.1
| TYPE: DNA
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                                                                                                                                                                                                                                                                                         Sequence 17771, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Lillie, Jamela
| APPLICANT: Lillie, Jamela
| APPLICANT: Lillie, Jamela
| TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND
| TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| FILE REPERENCE: MRI-0068
| CURRENT FILING DATE: 2001-03-21
| FRIOR APPLICATION NUMBER: US 60/191,031
| PRIOR FILING DATE: 2000-03-21
| PRIOR FILING DATE: 2000-05-25
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-07-07
| PRIOR FILING DATE: 2000-07-07
| PRIOR FILING DATE: 2000-07-07
| PRIOR FILING DATE: 2000-07-07
| PRIOR FILING DATE: 2000-07-25
| PRIOR FILING DATE: 2000-07-25
| PRIOR FILING DATE: 2000-07-25
| PRIOR FILING DATE: 2000-07-25
| PRIOR FILING DATE: 2000-07-25
| PRIOR APPLICATION NUMBER: US 60/257,672
| PRIOR APPLICATION NUMBER: US 60/257,672
| PRIOR PRIOR PRIOR PRIOR 2000-07-25
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1.5%; Score 25; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels
                                    1689 GTAAGTACCTCGGCGGGGACCACGC 1713
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                                                                                 428 GTAAGTACCTCGGCCGCGACCACGC 452
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ORGANISM: Homo sapiens
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US-10-477-45-15

US-10-477-45-15

Sequence 15, Application US/10477445

Publication No. US20050130138A1

GENERAL INFORMATION:

APPLICANT: Bayer AG

TITLE OF INVENTION: Immune-related proteins and the regulation of the same

FILE REFRENCE: RCK-12

CURRENT APPLICATION WIMBER: US/10/477,445

CURRENT FILING DATE: 2003-11-10

PRIOR FILING DATE: 2002-05-10

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 2001-05-11

WIMBER OF SEQ ID NOS: 111

SEQ ID NO 15
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             Sequence 1051, Application US/10950009
(BURDAL INFORMATION:
APPLICANT: BERKA, Randy
APPLICANT: BASHKIROVA, Elena
TITLE OF INVENTION: Methods
CURRENT APPLICATION WHENER: US/10/950,009
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: US/506,140
PRIOR PELING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1190
SOFTWARE: FESTERE 109-15
SOFTWARE: FESTERE OF Windows Version 4.0
SEQ ID NO 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 1.4%; Score 24; DB 9; Length 150; l Similarity 100.0%; Pred. No. 0.14; 24; Conservative 0; Mismatches 0; Indels
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
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LOCATION: 145.7145
OTHER INFORMATION: unknown nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 29
US-09-814-353-17222/c
; Sequence 17222, Application US/09814353
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; LOCATION: 231..231
; CTHER LIORATION: unknown nucleotide
US-10-477-445-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 TAAGTACCTCGGCCGCGACCACGC 1
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Trichoderma reesei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
JS-10-950-009-1051/c
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Query Match
1.4%; Score 24; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
PRIOR PLLING DATE: 2000-07-25
PRIOR PLLING DATE: 2000-17-25
PRIOR PLLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 13395
LENGTH: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1690 TAAGTACCTCGGCCGCGACCACGC 1713
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US-09-814-353-16395
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; ORGANISM: Homo sapiens
US-09-814-353-3678
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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Matches
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; Publication No. US20030165831A1
; GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANTON: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-0068
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT PILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR PILING DATE: 2000-06-25
; PRIOR APPLICATION NUMBER: US 60/211,940
                                                                                                                         Gaps
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Fublication No. US20030165831A1
GENERAL INRORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thillie, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: UMMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-27
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                                       DB 3; Length 274; 0.14;
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches
                                       Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 24; Conservative 0; Mismatches
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US-09-814-353-16395/c
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LENGTH: 274
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Sequence 36'8, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:
APPLICANT: Liblia Jamela
APPLICANT: Liblia Jamela
APPLICANT: Liblia Jamela
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION NUMBER: US 60/191,031
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PSECSE OF WINDOWS VETSION 4.0
SEQ ID NO 36'8

LEASTH: 310
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
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54 TAAGTACCTCGGCCGCGACCACGC 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, John APPLICANT: Thompson
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US-US-104-23-616, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Inilie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION UNMERR: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07
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GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KIT
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KIT
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE REPRENCE: MRI-006B
CURRENT FILING DATE: 2001-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: US 60/216, 820
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10381
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0.14;
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US-09-814-353-2976/c
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Fublication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Invertion: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: IDENTIFICATION, AND STILE OF INVENTION: IDENTIFICATION NUMBER: US 60/191,031

FRIOR FILING DATE: 2000-03-21

FRIOR FILING DATE: 2000-03-21

FRIOR FILING DATE: 2000-06-15

FRIOR FILING DATE: 2000-06-15

FRIOR FILING DATE: 2000-06-15

FRIOR FILING DATE: 2000-07-25

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                                            NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITION:
TITLE OF INVENTION: DIBNITETCATION, ASSESSM;
TITLE OF INVENTION: THERAPY OF OVARIAN CANC.
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-17-25
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 24; Conservative
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US-09-814-353-4074
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US-09-814-353-4074/c
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SEQ ID NO 4074
LENGTH: 312
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Publication No. US20040110668A1
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| Dublication No. US20030165831A1 |
| GENERAL INFORMATION: |
| APPLICANT: Lee, John |
| APPLICANT: Lee, John |
| APPLICANT: Lillie, James |
| APPLICANT: Lillie, James |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
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| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| FILE REFERENCE: MINORER: US 60/191,031 |
| PRIOR PILLING DATE: 2000-03-21 |
| PRIOR PILLING DATE: 2000-05-25 |
| PRIOR PILLING DATE: 2000-06-15 |
| PRIOR PILLING DATE: 2000-07-07 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR PILLING DATE
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1.4%; Score 24; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SECTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2976
LENGTH: 319
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9305
LENGTH: 319
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LCCATION: 181, 183, 191, 314

OTHER INFORMATION: n = A,T,C or G

US-09-814-333-9305
                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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; Sequence 1870, Application US/09969034

RESULT 39 US-09-969-034-1870

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Query Match 1.4%; Score 24; DB 3; Length 368; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASISEQ for Windows Version 4.0
SEG ID NO 4711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1690 TAAGTACCTCGGCCGCGACCACGC 1713
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 204
COTHER INFORMATION: n = A,T,C or G
US-09-814-353-11010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

1 LCCATION: 204

2 OTHER INFORMATION: n = A,T,C or G

US-09-814-333-4711
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ORGANISM: Homo sapiens
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US-10-370-7995/C

Sequence 7995, Application US/10357930

Publication No. US20040259086A1

Sequence 7995, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Endege, Wilson

APPLICANT: Endege, Wilson

APPLICANT: Endege, Wilson

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: UMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 06/183,319

PRIOR FILING DATE: 2000-02-17

PRIOR PELING DATE: 2000-02-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR PRILING DATE: 2000-07-18

PRIOR PRILING DATE: 2000-01-18

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Publication No. US20030165831A1

GENERAL INPORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Line, James
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Inhie, James
APPLICANT: Inhie, James
APPLICANT: US/09/814,353
TITLE OF INVENTION: THEAAPY OF OVARIAN CANCER
FILE REFERENCE: MR.-0068
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR PLING DATE: 2000-03-21
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                                                                                                    Length 326;
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                                                                                                                                                                   0; Indels
                                                                                                    DB 3;
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1.4%; Score 24; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches (
                                                                                                Query Match

1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                   1690 TAAGTACCTCGGCCGCGACCACGC 1713
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OTHER INFORMATION: n = A, T, C or G
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US-10-357-930-7995
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             ; OTHER INFORMATION OF 17947
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1.4%; Score 24; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
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Sequence 6066, Application US/10357930

Publication No. US20040259086A1

Sequence 6066, Application US/10357930

Publication No. US20040259086A1

SERERAL INFORMATION:

APPLICANT: Endege, Wilson

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMBER: US/10/357,930

CURRENT APPLICATION NUMBER: 05/18,276

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-02-16

PRIOR PELING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-06-05

PRIOR PELING DATE: 2000-06-05

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR PRIOR FILING DATE: 2000-06-07

PRIOR PRIOR FILING DATE: 2000-06-07

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PRIOR PRIOR FILING DATE: 2000-06-07

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0.14;
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 12238
; LENGTH: 370
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                                                                                                                                                                                                                                                           TYPE: DNA

ROGANISM: Homo sapiens

FRATURE:

NAME/KEY: misc_feature

LOCATION: 236, 252, 254, 313, 322, 329

COTHER INFORMATION: n = A,T,C or G

US-09-814-353-12238
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; ORGANISM: Homo sapiens
US-10-357-930-6066
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US-09-814-353-16765/c
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                                                                                                                                                                                WESOUR 193
UKS-09-814-353-12238/C
Sequence 12238, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, Jamela
APPLICANT: Lillie, Jamela
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: US/09/814,353
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/21,124
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
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1.4%; Score 24; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
  1690 TAAGTACCTCGGCCGCGACCACGC 1713
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; LOCATION: 236, 252, 254, 313, 322, 329
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5958
                             30 TAAGTACCTCGGCGCGACCACGC 7
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ORGANISM: Homo sapiens
                                                                                                                                            RESULT 44
US-09-814-353-5958/c
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Gaps

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APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Dames
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAFY OF COVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PALICATION NUMBER: US 60/207,124
PRIOR PLING DATE: 2000-05-25
PRIOR PAPLICATION NUMBER: US 60/207,124
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-07-22
PRIOR FILING DATE: 2000-07-22
PRIOR PLING DATE: 2000-07-22
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PLING DATE: 2000-07-22
PRIOR PLING DATE: 2000-07-22
PRIOR PLING DATE: 2000-07-22
PRIOR PLING DATE: 2000-07-22
PRIOR PLING DATE: 2000-07-22
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APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, James
APPLICANT: Thompson, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-068
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US/0191,031
PRIOR APPLICATION NUMBER: US/0191,031
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: US/000-05-25
PRIOR PILING DATE: US/000-05-25
                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 391;
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0.14;
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                                                                                                                                                                                                              1690 TAAGTACCTCGGCCGCGACCACGC 1713
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Publication No. US20030165831A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                               30 TAAGTACCTCGGCGCGCACCACGC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9231, Application US/09814353
Publication No. US:0030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-814-353-9231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-814-353-16375/c
                                                                                                                                                                                                                                                                                                                                                                            RESULT 49
US-09-814-353-9231/c
          US-09-814-353-2902
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APPLICANT: Thompson, Pamela
TITLE OF INVENTION: NOVELE GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVELE GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 22037
SUPPLICATION NUMBER: US 60/257,672
                                                                                                                                                      APPLICANT: INCOMEDIA, AGREEA

APPLICANT: INTINE, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MKI-0668

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-25

PRIOR PELICATION NUMBER: US 60/216,820

PRIOR FILING DATE: 2000-07-25

PRIOR PELICATION NUMBER: US 60/220,661

PRIOR FILING DATE: 2000-07-25

PRIOR PELING DATE: 2000-07-25

PRIOR PELING DATE: 2000-17-25

NUMBER OF SEC ID NOS: 22037

SOFTWARRE FRASERE FRASERE FOR WINGOWE VEFRION 4.0

SEQ ID NO 16765

LINGTHE LINES DATE: 2000-17-25

HUMBER OF SEC ID NOS: 22037

TWOIL NAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1690 TAAGTACCTCGGCCGCGACCACGC 1713
Sequence 16765, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 TAAGTACCTCGGCCGCGACCACGC 78
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; Sequence 2902, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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WESULT 51

WESULT 51

Sequence 3267, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-006B

CURRENT PEPLICANTION NUMBER: US/09/814,353

CURRENT PEPLICATION NUMBER: US 60/191,031

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-07-07

PRIOR PELING DATE: 2000-07-07

PRIOR PELING DATE: 2000-07-25

PRIOR PELING DATE: 2000-07-25

PRIOR PELING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR PELING DATE: 2000-07-25

PRIOR PELING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 22037

SECOND DATE: 2000-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.4%; Score 24; DB 3; Length 391; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FRALSEQ for Windows Version.4.0
SEQ ID NO 16375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1690 TAAGTACCTCGGCCGCGACCACGC 1713
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) LOCATION: 327, 378, 384

; CTHER INFORMATION: n = A,T,C or G

US-09-814-353-3267
                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-814-353-16375
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ORGANISM: Homo sapiens
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LENGTH: 392
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RESULT 52 US-09-814-353-9592/c

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KESULY 56
US-09-814-353-5221/C
| Sequence 521, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Lee, John
| APPLICANT: Lille, James
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NUMBER: US/09/814,353
| CURRENT APPLICATION NUMBER: US 60/201,031
| PRIOR FILING DATE: 2000-03-21
| PRIOR PELICATION NUMBER: US 60/201,940
| PRIOR FILING DATE: 2000-06-15
| PRIOR PELICATION NUMBER: US 60/211,940
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-07-25
| PRIOR APPLICATION NUMBER: US 60/257,672
| PRIOR APPLICATION NUMBER: US 60/257,672
| PRIOR APPLICATION NUMBER: US 60/257,672
| PRIOR APPLICATION NUMBER: US 60/257,672
| PRIOR APPLICATION NUMBER: US 60/257,672
| PRIOR SEQ ID NOS: 22037
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 5221
| LENGTH: A16
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      IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
                                    THERAPY OF OVARIAN CANCER
                                                        THILE REPERENCE: MRI-066B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/201,940
PRIOR PILING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEC ID NOS: 22037
SEC ID NO 17159
LENGTH: 415
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CORGANISM: Homo sapiens
US-09-814-353-17159
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LOCATION: 271
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APPLICANT: Thompson, kameta
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS POR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS POR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2001-03-21
PRIOR PLING DATE: 2000-03-22
PRIOR PLICATION NUMBER: US 60/207,124
PRIOR PLICATION NUMBER: US 60/201,940
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-07-07
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.4%; Score 24; DB 8; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
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Matches 24; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8043
LENGTH: 404
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Publication No. US20030165831A1
GENERAL INFORMATION:
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                              | NAME/KEY: misc_feature
| LCCATION: 37, 54, 147
| CTHER INFORMATION: n = A,T,C or G
| US-10-357-930-8043
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APPLICANT: Thompson, Pamela
                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-09-814-353-17159/c
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DB 3; Length 420; 0.13;
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100.0%; Pred. No. 0.13;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                 Query Match
1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PastSEQ for Windows Version 4.0
SEGID NO 12779
                                                                                                                                                                                                                                                                                                                                                                                                                 1690 TAAGTACCTCGGCCGCGACCACGC 1713
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Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-814-353-12779
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US-09-814-353-5813
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                                                                                                                                                                                                 Sequence 11508, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lillib. James
| APPLICANT: Lillib. James
| APPLICANT: Lillib. James
| APPLICANT: Lillib. James
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF OVARIAN CANCER
| TITLE OF INVENTION: IDENTIFICATION, AND STILLS PRICATION NUMBER: US 60/191,031
| PRIOR FILLING DATE: 2000-03-21
| PRIOR FILLING DATE: 2000-06-15
| PRIOR PELICATION NUMBER: US 60/210,940
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-07-27
| PRIOR FILING DATE: 2000-07-27
| PRIOR PELICATION NUMBER: US 60/257,672
| PRIOR PILING DATE: 2000-12-21
| PRIOR FILING DATE: 2000-12-21
| NUMBER OF SEQ ID NOS: 22037
| SOFTWARE: PRESENCE OF WINDOWS VERSION 4.0
| SEQ ID NO 11508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12779, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INPORMATION:
; GENERAL INPORMATION:
; APPLICANT: Let, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILLS REPRESENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-03-21
                             Gaps
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                             0; Indels
    Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches
                                                                   1690 TAAGTACCTCGGCCGCGACCACGC 1713
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US-09-814-353-11508
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LOCATION: 271
                                                                                                                                                                   RESULT 57
US-09-814-353-11508/c
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US-09-814-353-12779
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; Sequence 5813, Application US/09814353; Publication No. US20030165831A1; GENERAL INFORMATION:
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RESULT 62
US-10-198-846-7580/c
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Sequence 39249, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Endege, Wilson

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

ITILE OF INVENTION: NUMBER GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: HUMAN PROSITIONS, KITS, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSITIONS, KITS, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSITIONS, KITS, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSITIE CANCER

FILE REPREBENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: 09/785, 276

PRIOR FILING DATE: 2003-02-04

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/183, 319

PRIOR FILING DATE: 2000-03-16

PRIOR PLING DATE: 2000-06-05

PRIOR PELING DATE: 2000-06-05

PRIOR PLING DATE: 2000-06-09

PRIOR PLING DATE: 2000-06-09

PRIOR PLING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR PLING DATE: 2000-06-09

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR PRIOR FILING DATE: 2000-01-18

PRIOR PRIOR PRICEATION NUMBER: 60/255,281
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APPLICANT: Thompson, Pamela
APPLICANT: Lilite, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
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CURRENT PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-15

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-17-25

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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 39249
LENCTH: 424
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US-09-814-353-5813
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US-10-357-930-39249/c
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; ORGANISM: Homo :
US-10-357-930-39249
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US-09-814-353-18496/C

Sequence 18496, Application US/09814353

PUBLication No. US2030165831A1

GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Illile, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DEBYTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT FALLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191, 031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
                                                                                                                                                                                                                                                                                                                                           US-LICITES HEAD-/NBU/C

Sequence 7580, Application US/10198846

Publication No. US2030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Wangy vouchen

APPLICANT: Wangy Youchen

APPLICANT: Wangy Youchen

APPLICANT: Steinmann, Kathleen

FILE OF INVENTION: FOR IDENTIFICATION, AND MERS: US/10/198,846

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: US/10/198,846

FRIOR APPLICATION NUMBER: US/10/198,846

FRIOR APPLICATION NUMBER: US/10/198,846

FRIOR PILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7580
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DB 8; Length 424;
0.13;
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                                                                  0; Indels
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1.4%; Score 24; DB 5;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 24; Conservative 0; Mismatches
                                                                                                                               1690 TAAGTACCTCGGCCGCGACCACGC 1713
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LCCATION: 384

CTHER INFORMATION: n = A,T,C or G

US-10-198-846-7580
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US-10-357-930-37944/c
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Sequence 6566, Application US/10157930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DEDNIFICATION, AND THERAPY OF
TITLE OF INVENTION: DEDNIFICATION, AND THERAPY OF
TITLE OF INVENTION: UNMER: US/10/357,930
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-013-16
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-12
PRIOR PRIOR APPLICATION NUMBER: 60/255,281
PRIOR PRIOR DATE: 2000-01-12
PRIOR PRIOR DATE: 2000-01-12
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                       Query Match 1.4%; Score 24; DB 3; Length 426; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18496
LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 TAAGTACCTCGGCCGCGACCACGC 7
                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-814-353-18496
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Best Local Similarity
Matches 24; Conserva
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US-09-814-353-18622/c
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Gaps

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1.4%; Score 24; DB 3; Length 437;
100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9426
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| FRATURE:
| NAME/KEY: misc_feature
| LOCATION: 182, 223, 225, 281, 285, 392
| OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9426
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209-814-353-15845/c

; Sequence 15845, Application US/09814353

; Publication No. US20030165831A1
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Local Similarity 100.0%; P:
nes 24; Conservative 0;
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Matches 24; Conservative
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                                                                                                                                                                                                                     Sequence 3100, Application US/09814353
Fublication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lev, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: I.ilie, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: DATE: 2001-03-21
FRIOR PELING DATE: 2000-03-21
FRIOR PELING DATE: 2000-05-25
FRIOR PELING DATE: 2000-06-15
FRIOR PELING DATE: 2000-06-15
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FRIOR PELING DATE: 2000-06-15
FRIOR PELING DATE: 2000-07-27
FRIOR PELING DATE: 2000-07-27
FRIOR PELING DATE: 2000-07-25
FRIOR FILING DATE: 2000-07-27
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US-09-814-353-9426/c
Sequence 9426, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: US-09/814,353
CURRENT APPLICATION NUMBER: US-09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
          1690 TAAGTACCTCGGCCGCGACCACGC 1713
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; CCCATION: 182, 223, 225, 281, 285, 392
; CTHER INFORMATION: n = A,T,C or G
US-09-814-353-3100
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ORGANISM: Homo sapiens
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Sequence 18016, Application US/09814353

| Sequence 18016, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Lee, John
| APPLICANT: Lillie, James
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| FILE REFERENCE: MRI-066B
| CURRENT APPLICATION NUMBER: US 60/191,031
| PRIOR FILING DATE: 2000-03-21
| PRIOR PELICATION NUMBER: US 60/207,124
| PRIOR PELICATION NUMBER: US 60/211,940
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-07-25
| PRIOR PELICATION NUMBER: US 60/220,661
| PRIOR FILING DATE: 2000-07-25
| PRIOR FILING DATE: 2000-07-27
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Pred. No. 0.13;
0; Mismatches
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i LOCATION: 324
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4306
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APPLICANT: Lee, John Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPRENENCE: X10-066
CURRENT PLING DATE: 2001-03-21
PRIOR FILLING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR FILLING DATE: 2000-05-25
PRIOR FILLING DATE: 2000-05-25
PRIOR PLILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SEQ ID NO 4306
FROMTWARE: PARESEQ FOR WINDOWS VERSION 4.0
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                                                    APPLICANY: Thompson, Pamela
APPLICANY: Thompson, Pamela
APPLICANY: Thompson, Pamela
APPLICANY: Lillie, James
APPLICANY: Lillie, James
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: IDEATIFICATION, ASSESSMENT, PREVENTION, AND
ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT PELLING DATE: 2001-03-21
FRIOR PELLING DATE: 2000-03-21
FRIOR PELLING DATE: 2000-03-21
FRIOR PELLING DATE: 2000-05-25
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US-09-814-353-4306/c
Sequence 4306, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 36059, Application US/10357930

Sequence 36059, Application No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Bridege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: UNIVENTION: UNIVENTION: AND THERAPY OF

TITLE OF INVENTION: UNIVENTION: UNIVENTION: US/10/357,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10610, Application US/09814353

Sequence 10610, Application US/09814353

Publication No. U520030165831A1

GENERAL INPORMATION:

APPLICANT: Lee, John

APPLICANT: Lillie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, CONPOSITIONS, KITS, AND

FILE REFERENCE: REL.

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 2000-07-27

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PRIOR FILING DATE: 2000-07-27
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1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
Length 446;
                                                                                           0; Indels
DB 3;
. 0.13;
    Query Match
1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
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US-09-814-353-10610
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71 TAAGTACCTCGGCGCGCGACCACGC 48
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US-10-001-857-66
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APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE
TITLE OF INVENTION: HUMAN PROSTATE
CURRENT APPLICATION NUMBER: 09/185,276
PRIOR PELICATION NUMBER: 09/183,319
PRIOR PLING DATE: 2003-02-17
PRIOR PELICATION NUMBER: 60/183,319
PRIOR PLING DATE: 2000-02-17
PRIOR PLING DATE: 2000-03-16
PRIOR PLING DATE: 2000-03-16
PRIOR PLING DATE: 2000-03-16
PRIOR PLING DATE: 2000-05-16
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-12-13
PRIOR PLING DATE: 2000-12-13
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100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
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1.4%; Score 24; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR PILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR PILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PASSES FOR WINDOWS VERSION 4.0
SSOFTWARE: PASSES FOR WINDOWS VERSION 4.0
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APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 TAAGTACCTCGGCCGCGACCACGC 78
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Matches 24; Conservative
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; ORGANISM: Homo sapiens
US-10-357-930-37991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 74
US-10-357-930-37991/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-357-930-36059
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APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TILLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
SEQ ID NO 66
LENGTH: 457
                                                                                                                                                                                                                                           APPLICANT: SCHLEGEL.
APPLICANT: Budege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES,
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: WIMBER: CANCER
TITLE OF INVENTION: WIMBER: 09/785,7930
CURRENT FILING DATE: 2003-02-04
FRICH PELICATION NUMBER: 09/785,276
FRICH PELICATION NUMBER: 09/785,276
FRICH PELICATION NUMBER: 60/183,319
FRICH FILING DATE: 2000-02-17
FRICH PELICATION NUMBER: 60/189,862
FRICH PELICATION NUMBER: 60/207,454
FRICH FILING DATE: 2000-06-25
FRICH FILING DATE: 2000-06-25
FRICH PELICATION NUMBER: 60/211,314
FRICH FILING DATE: 2000-06-09
FRICH FILING DATE: 2000-06-09
FRICH FILING DATE: 2000-06-12
FRICH FILING DATE: 2000-07-18
FRICH FILING DATE: 2000-07-18
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1.4%; Score 24; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
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                                                                            Sequence 45120, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
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US-10-001-857-66/c
; Sequence 66, Application US/10001857
; Publication No. US20020183500A1
; GENRRAL INFORMATION:
; APPLICANT: Macina, Roberto
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RESULT 75
US-10-357-930-45120/c
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Length 463; Indels

DB 5; 0.13;

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; TYPE: DNA

; GRGANISH: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 18, 43, 86, 89, 264, 388, 407, 432

; STHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                             Query Match

1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     1690 TAAGTACCTCGGCCGCGACCACGC 1713
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 79
US-09-814-353-3344/c
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US-10-198-846-5501/c
US-10-198-846-5501, Application US/10198846

| Publication No. US20030099974A1
| GENERAL INFORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Lillie, James
| APPLICANT: Lillie, James
| APPLICANT: Steinmann, Kathleen
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| FILE REPERENCE: MRI-049
| CURRENT FILING DATE: 2002-07-18
| PRIOR APPLICATION NUMBER: 60/200-07-18
| PRIOR APPLICATION NUMBER: 60/306,220
| PRIOR APPLICATION NUMBER: 60/306,220
| PRIOR SEQ ID NOS: 140084
| SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                      WES-09-614-353-18705/c

Sequence 18705, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-0068

CURRENT FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-07

PRIOR PLING DATE: 2000-07-07

PRIOR PLING DATE: 2000-07-22

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PRIOR PLING DATE: 2000-07-22
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Score 24; DB 5; Length 457;
Pred. No. 0.13;
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0.13;
Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 24; Conservative 0; Mismatches
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
                                                                                                                        1690 TAAGTACCTCGGCCGCGACCACGC 1713
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LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,
LOCATION: 383, 393, 417, 422, 428, 431
OTHER INFORMATION: n = A,T,C or G
                                                                                           APPLICANT: Lee, John
APPLICANT: Lillie, Jamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
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1.4%; Score 24; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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FRIOR APPLICATION UNWBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-25

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

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PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-15

PRIOR PILING DATE: 2000-07-15

PRIOR PILING DATE: 2000-07-15

PRIOR PILING DATE: 2000-07-15

PRIOR PILING DATE: 2000-12-1

NUMBER OF SEQ ID NOS: 22037

SEQ ID NO 3344

LENGTH: 464
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Sequence 3344, Application US/09814353 Publication No. US20030165831A1 GENERAL INFORMATION:
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APPLICANT: Thompson, Pame
APPLICANT: Lillie, James
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RESULT 82
US-09-814-353-4472/c
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US-09-814-353-15851/C
Sequence 15851, Application US/09814353
; Publication No. US20030165831A1
GENERAL INPORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thilie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-0068
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-0068
CURRENT FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/201,124
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR FILING 
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND FILL GO INVENTION: THERAPY OF OVARIAN CANCER FILE REFERENCE: MRI-0668

CURRENT FILING DATE: 2001-03-21

PRIOR PLICATION NUMBER: US 60/191,031

PRIOR PLICATION NUMBER: US 60/191,031

PRIOR PLICATION NUMBER: US 60/207,124

PRIOR PLICATION NUMBER: US 60/207,124

PRIOR PLICATION NUMBER: US 60/207,124

PRIOR PLICATION NUMBER: US 60/211,940

PRIOR PLICATION NUMBER: US 60/216,820

PRIOR PLICATION NUMBER: US 60/220,661

PRIOR PLICATION NUMBER: US 60/220,661

PRIOR PLICATION NUMBER: US 60/220,661

PRIOR PLING DATE: 2000-07-25

PRIOR PLING DATE: 2000-07-22

NUMBER OF SEQ ID NOS: 22037

SOFTWARE: PRACESQ for Windows Version 4.0

SEQ ID NO 9665
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; LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,

; LOCATION: 383, 393, 403, 417, 422, 428, 431

; COTHER INFORMATION: n = A,T,C or G

US-09-814-353-9665
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Best Local Similarity 100.0
Matches 24, Conservative
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; ORGANISM: Homo sapiens
US-09-814-353-15851
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US-09-814-353-15976/c
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US-09-814-353-4993/C
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                Matches
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APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR PILING DATE: 2001-03-21
PRIOR PLILING DATE: 2000-05-25
PRIOR PLILING DATE: 2000-06-25
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
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PRIOR PLILING DATE: 2000-07-07
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PRIOR PLILING DATE: 2000-07-25
PRIOR PLILING DATE: 2000-12-21
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; LOCATION: 31, 98, 159, 166, 289, 348, 361, 364, 385, 393, 398, 400,

; LOCATION: 410, 414, 419, 432, 457, 467

; OTHER INFORMATION: n = A,T,C or G

US-09-814-353-10775
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1.4%; Score 24; DB 3; Length 486;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 10775
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16367
LENGTH: 503
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
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US-09-814-353-16367
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US-09-814-353-16367/c
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Sequence 15615, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
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| Sequence 11286 | Application US/09814353 |
| Publication No. US20303165831A1 |
| GENERAL INFORMATION: |
| APPLICANT: Lee, John |
| APPLICANT: Thompson, Pamela |
| APPLICANT: Inilie, James |
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: OF OVARIAN CANCER |
| FILE REFERENCE: MAI-0068 |
| CURRENT APPLICATION NUMBER: US 60/191, 031 |
| PRIOR FILING DATE: 2000-03-21 |
| PRIOR FILING DATE: 2000-05-25 |
| PRIOR FILING DATE: 2000-06-15 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR APPLICATION NUMBER: US 60/216, 820 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR APPLICATION NUMBER: US 60/257, 672 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR FILING DATE: 2000-07-07 |
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1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FRALSEQ for Windows Version 4.0
SEQ ID NO 4993
LENGTH: 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1690 TAAGTACCTCGGCCGCGACCACGC 1713
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LOCATION: 443, 491
OTHER INFORMATION: n = A,T,C or G
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i_LOCATION: 443, 491
COTHER INFORMATION: n = A,T,C or G
US-09-814-353-11286
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-814-353-11286/c
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RESULT 88 US-09-814-353-15615/c

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GENERAL LINCURANT: LOW:

APPLICANT: Lie, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, Jame
ITILE OF INVENTION: IDENTIPICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MRI-066B
CURRENT FILING DATE: 2001-03-21
FRICA PLICATION NUMBER: US 60/191,031
PRIOR PLICATION NUMBER: US 60/207,124
PRIOR PLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR PLICATION NUMBER: US 60/220,661
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US-09-814-353-17892/C

Sequence 17892, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, Jameson, ASESSMENT, PREVENTION, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-066B
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-07-25
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches (
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ORGANISM: Homo sapiens
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APPLICANT: Lie, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lille, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: US 60/291,031
PRIOR PLICATION NUMBER: US 60/207,124
PRIOR PLICATION NUMBER: US 60/211,940
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-15
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
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PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-17-21
NUMBER OF SEQ ID NOS: 22037
SEQ ID NO 5823
LINGGARE PRESEQ FOR WINGOWE VETRION A.N.
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
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                                                                                                                                                                       1.4%; Score 24; DB 3; Length 524; 100.0%; Pred. No. 0.13; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                      1690 TAAGTACCTCGGCCGCGACCACGC 1713
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Publication No. US20030165831A1
GENERAL INFORMATION:
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 350
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-17892
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; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5823
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Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                 Best Local Similarity 100.
Matches 24; Conservative
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US-09-814-353-12105/c
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US-09-814-353-5823/c
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APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERRY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLING DATE: 2000-07-07
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100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 12105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 435
OTHER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: n = A,T,C or G
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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US-09-814-353-17394/c
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Sequence 39396, Application US/10357930

Sequence 39396, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-00736CN

CURRENT APPLICATION NUMBER: 09/785,276

PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/213,314

PRIOR APPLICATION NUMBER: 60/210,007

PRIOR APPLICATION NUMBER: 60/210,007

PRIOR APPLICATION NUMBER: 60/210,007

PRIOR APPLICATION NUMBER: 60/210,007

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PRIOR PRIOR APPLICATION NUMBER: 60/210,007

PRIOR PRIOR APPLICATION NUMBER: 60/210,007

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FASTSEQ for Windows Version 4.0
SCOTUD NO 12321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1690 TAAGTACCTCGGCCGCGACCACGC 1713
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NAME/KEY: misc_feature

LOCATION: 388, "442, 468, 478, 503, 540

CTHER INFORMATION: n = A,T,C or G

US-09-814-353-12321
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Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-357-930-39396/c
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| Sequence 6042, Application US/09814353|
| US-09-814-353-6042/c
| Sequence 6042, Application US/09814353|
| Publication No. US20030165831A1 |
| GENERAL INFORMATION: | GENERAL INFORMATION: | APPLICANT: Lee, John |
| APPLICANT: Lille, James |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| FRICA FILING DATE: 2000-03-21 |
| PRIOR FILING DATE: 2000-03-21 |
| PRIOR FILING DATE: 2000-03-21 |
| PRIOR FILING DATE: 2000-05-25 |
| PRIOR FILING DATE: 2000-05-25 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR FILING DATE: 2000-07-07 |
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MIL-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US (00191,031
PRIOR PILING DATE: 2000-03-21
                                                                                                                                         Gaps
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                                            Query Match 1.4%; Score 24; DB 3; Length 546; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches 0; Indels
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Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                             1690 TAAGTACCTCGGCCGCGACCACGC 1713
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) LOCATION: 388, 442, 468, 478, 503, 540

) OTHER INFORMATION: n = A,T,C or G

US-09-814-353-6042
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US-09-814-353-12321/c
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RESULT 98
US-10-357-930-36049
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                                                                                                                                       Sequence 43996, Application US/10357930

Sequence 43996, Application US/10357930

GENERAL INPORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMBER: US/10/357,930
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT PILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR PELING DATE: 2000-03-16
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-25
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PRIOR PELING DATE: 2000-05-18
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PRIOR PELING DATE: 2000-05-31
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| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lef. John
| APPLICANT: Thompson, Pamela
| APPLICANT: Thompson, Pamela
| APPLICANT: Lillie, James
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| FILE REFERENCE: MRI-0.068
| CURRENT APPLICATION NUMBER: US/09/814,353
| CURRENT PILING DATE: 2001-03-21
| PRIOR PPLICATION NUMBER: US 60/191,031
| PRIOR FILING DATE: 2000-05-25
| PRIOR PLILING DATE: 2000-05-25
| PRIOR PLILING DATE: 2000-06-15
| PRIOR PLILING DATE: 2000-06-15
| PRIOR APPLICATION NUMBER: US 60/211,940
| PRIOR PLILING DATE: 2000-06-07-07
| PRIOR APPLICATION NUMBER: US 60/216,820
| PRIOR APPLICATION NUMBER: US 60/220,661
| PRIOR APPLICATION NUMBER: US 60/220,661
| PRIOR PLILING DATE: 2000-07-25
| PRIOR PRIOR APPLICATION NUMBER: US 60/257,672
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85 TAAGTACCTCGGCCGCGACCACGC 62
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US-09-814-353-18489/c
                                                                                         RESULT 96
US-10-357-930-43996/c
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Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITIONS, KITS, AND METHODS FOR
ASSESSMENT, PREVENTION, AND THERAPY OF
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                                                                                                                                                                                                                                                                                            Length 601;
                                                                                                                                                                                                                                                                                                                                                          0; Indels
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36049, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Schlege, Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT PELLING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/795,276
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PRAELES FOR WINDOWN VERSION 4.0
SEQ ID NO 36049
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FRSESEQ for Windows Version 4.0
; SEQ ID NO 18489
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18489
                                                                                                                                                                                                                                                                                                                                                                                                                     1690 TAAGTACCTCGGCCGCGACCACGC 1713
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ORGANISM: Homo sapiens
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US-10-950-009-112/c
; Sequence 112, Application US/10950009
; Publication No. US20050669914A1
; GENERAL INFORMATION:
    APPLICANT: BERKA, Randy
; APPLICANT: BASKHINOVA, Elena
APPLICANT: REY, Michael
; TITLE OF INVENTION: Methods For Monitoring Gene Expression
FILE REFERENCE: 10541.200-US
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/506,140
PRIOR APPLICATION NUMBER: 60/506,140
; SUGTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 112
; LENGTH: 610
; TYPE: DNA
; ONGANISM: Trichoderma reesei
US-10-950-009-112
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1.4%; Score 24; DB 8; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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1.4%; Score 24; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
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CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/786,276
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PRIOR FILING DATE: 2000-07-18
PRIOR PLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62223
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CORGANISM: Homo sapiens
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Search completed: March 11, 2006, 22:31:51 Job time : 1455 secs

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; Publication No. US20060003322A1
; Publication No. US20060003322A1
; GENERAL INFORMATION:
    APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectal; TITLE OF INVENTION: Bioinformatically detectal; TITLE OF INVENTION: uses thereof; FILE REFERRNCE: 06097, 0200, CEDUSO1; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR PELLING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SEQ ID NO 799
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Best Local Similarity 99.9
Matches 1694; Conservative
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Deblication No. US20050272080A1

Squence 344331, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION:

Microarrays

FILE REPERENCE: 3684.1

CURRENT FILING DATE: 2005-05-03

PRIOR PAPLICATION NUMBER: US/11/121,849

PRIOR PAPLICATION NUMBER: 05/567,949

PRIOR PAPLICATION NUMBER: 06/567,949

PRIOR PAPLICATION NUMBER: 06/567,949

PRIOR PAPLICATION NUMBER: 06/567,949

REAL OF THE DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NO 344331

LENGTH: 25
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Publication No. US20050272080A1

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.11

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR PAPLICATION NUMBER: 60/567,949

PRIOR PELLON PRIOR PARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 344332

LENGTH: 25
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
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; Sequence 344333, Application US/11121849
; Publication No. US20050272080A1
    1 CTGGACCATGTGCATTTCACTGGGC 25
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Best Local Similarity 100.
Matches 25; Conservative
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Matches 25; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-344332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapien
US-11-121-849-344331
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                                                                                                   US-11-121-849-344331
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Publication No. US20060003322A1
Publication No. US2006000332A1
Publication No. US2006000332A1
Publication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Wuzat
APPLICANT: Shiler, Wuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045320
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Publication No. US20050272080A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded (
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION NUMBER: US/11/121,849
FILE REFERENCE: 3684-05-03
CURRENT APPLICATION NUMBER: GO/567,949
FRIOR PLING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 34330
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                                                                                                                                                                                            Length 25;
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100.0%; Pred. No. 0.028;
tive 0; Mismatches 0
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1... 0; Mismatches
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045304
LENGTH: 25
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Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity 100.
Matches 25; Conservative
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US-11-121-849-344330
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-10-310-914A-1045320/c
                                                                                            ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045304
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Sequence 344336, Application US/11121849
; Sequence 344336, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
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TITLE OF INVENTION: Microarray
FRIOR APPLICATION NUMBER: 60/567,949
FRIOR APPLICATION NUMBER: 60/567,949
FRIOR FILING DATE: 2004-05-03
FRIOR APPLICATION OF SEQUENCE Listing Generator V 1.1
SEQ ID NO 344336
LENGTH: 25
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Sequence 344337, Application US/11121849
Fublication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
FRIOR PELICATION NUMBER: 60/567,949
FRIOR PELICATION NUMBER: 60/567,949
FRIOR PELICATION NOWBER: 60/567,949
FRIOR PELICATION NOWBER: 60/567,949
FRIOR PELICATION NOWBER: 5004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344337
ILENGTH: 25
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Pred. No. 0.028;
          0; Mismatches
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                                                          1466 AGGAGTTAGGCATTACCTTCTGGGA 1490
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                                                                                                             1 AGGAGTTAGGCATTACCTTCTGGGA 25
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        25; Conservative
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US-11-121-849-344336
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; ORGANISM: Homo sapien
US-11-121-849-344337
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     Matches
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Sequence 344334, Application US/11121849
Sequence 346314, Application US/11121849
Sequence 346314, Application US/11121849
Sequence 346314
Sequence 346314
Sequence 346314
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344334
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Publication No. US2005027208041

GENERAL INPORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION NUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: US/657,949

PRIOR APPLICATION NUMBER: Q0/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NOS: 673904

SEQ ID NO 344335

LENGTH: 25
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CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE MICROALRAY Probe Sequence Listing Generator V 1.1
SEQ ID NO 344333
LENGTH: 25
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100.0%; Pred. No. 0.028;
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Best Local Similarity 100.0
Matches 25; Conservative
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Matches 25; Conservative
                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapien
US-11-121-849-344333
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; ORGANISM: Homo sapien
US-11-121-849-344334
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ORGANISM: Homo sapien
US-11-121-849-344335
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Best Local Similarity
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US-11-121-849-344334
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US-11-121-849-344335
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344517
LENGTH: 25
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Sublication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Statile OF INVENTION:
Microarrays
FILE REFERENCE: 3684.1
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
FRIOR FILING DATE: 2004-05-03
FRIOR FILING DATE: 2004-05-03
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                                                1.5%; Score 25; DB 12; Length 25; 100.0%; Pred. No. 0.028; ive 0; Mismatches 0; Indels
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344518
LENGTH: 25
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100.0%; Pred. No. 0.028;
tive 0; Mismatches 0
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Publication No. US20050272080A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 25; Conservative
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CORGANISM: Homo sapien
US-11-121-849-344517
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US-11-121-849-344518
                                                  Query Match
Best Local Similarity
Matches 25; Conserv
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US-11-121-849-344519
            US-11-121-849-344340
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US-11-121-849-344340
US-11-121-849-344340, Application US/11121849
Publication No. US205050272080A1
Publication No. US205050272080A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
NUMBER OF SEQ ID NOS: 673904
SOSTWARE: Microarray Probe Sequence Listing Generator V 1.1
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays
FILE REPERENCE: 3684.1

CURRENT APPLICATION NUMBER: 06/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: McCroarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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100.0%; Pred. No. c.
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Matches 25, Conservative
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Best Local Similarity 100.
Matches 25, Conservative
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CRGANISM: Homo sapien
US-11-121-849-344338
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; ORGANISM: Homo sapien
US-11-121-849-344339
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ORGANISM: Homo sapien
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US-11-121-849-344339
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LENGTH: 25
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Sequence 344523, Application US/11121849
Sequence 344523, Application US/11121849
Sequence 344523, Application No. US20056272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
FILE REFRENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
FRIOR APPLICATION NUMBER: 60/567,949
FRIOR PELING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NO 344523
LENGTH: 25
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                                                                                                                                          Query Match 1.5%; Score 25; DB 12; Length 25; Best Local Similarity 100.0%; Pred. No. 0.028; Matches 25; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.028;
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0.028;
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1.5%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 25; Conservative
                                                   TYPE: DNA
CORGANISM: Homo sapien
US-11-121-849-344521
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US-11-121-849-344522
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US-11-121-849-344523
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US-11-121-849-344522
         ; SEQ ID NO 344521
; LENGTH: 25
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Sequence 344519, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Mcroarrays
TITLE OF INVENTION: Mcroarrays
FILE REPERBNCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT PILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344519
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US-11-121-849-344520
US-11-121-849-344520
Sequence 344520, Application US/11121849
Sequence 344520, Application No. US20050272080A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR PRILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION UMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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100.0%; Pred. No. 0.028;
tive 0; Mismatches 0; Indels
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344520
LENGTH: 25
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US-11-121-849-344521
; Sequence 344521, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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Matches 25, Conservative
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; ORGANISM: Homo sapien
US-11-121-849-344519
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US-11-121-849-344520
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Matches 25; Conserv
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Sequence 344527, Application US/11121849
Sequence 344527, Application US/11121849
Sequence 344527, Application No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Static OF INVENTION: Microarrays
TITLE OF INVENTION:
MICROBIA APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
CURRENT FILING DATE: 2006-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NO 344527
LENGTH: 25
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Publication No. US2060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Biler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087,0200, CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT APPLICATION WUMBER: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045318
LENGTH: 24
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PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673804
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344526
LENGTH: 25
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Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344526
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CORGANISM: Homo sapien
US-11-121-849-344527
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US-10-310-914A-1045318/c
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Publication No. US20050272080A1
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Publication No. U320050272080A1
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Sequence 344526, Application US/11121849

Sequence 344526, Application US/11121849

Sequence 344526, Application US/11121849

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03
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100.0%; Pred. No. 0.028;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. v.
0; Mismatches
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Best Local Similarity 100.
Matches 25; Conservative
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Matches 25; Conservative
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US-11-121-849-344524
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; ORGANISM: Homo sapien
US-11-121-849-344525
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US-11-121-849-344525
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Sequence 1045327, Application US/10310914A

Publication No. US20060003322A1

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Publication No. US20060003322A1
Publication No. US20060003322A1
Publication No. US2006000332A1
Rubication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045337
LENGTH: 23
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100.0%; Pred. No. 0.3
:ive 0; Mismatches
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1.3%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 23; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SSCTWARE: Patentin version 3.3 SEQ ID NO 1045322 LENGTH: 23
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Best Local Similarity 100.0
Matches 23; Conservative
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Baac
APPLICANT: Bentwich, Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045311
                                                                                                                                                                                                                                 Sequence 1045328, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANTON: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045328
LENGTH: 24
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) Publication No. US20060003322A1
) GENERAL INFORMATION:
| APPLICANT: Bentwich, Kruzat
| APPLICANT: Shiler, Kruzat
| TITLE OF INVENTION: Uses thereof
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100.0%; Pred. No. 0.093;
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Pred. No. 0.3;
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   1378 ATCTCCTTGCATCCCCAGCTGGTC 1401
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Best Local Similarity 100.
Matches 24; Conservative
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US-10-310-914A-1045328/c
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US-10-310-914A-1045322/c
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US-10-310-914A-1045311/c
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; ORGANISM: Human
US-10-310-914A-1045328
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ORGANISM: Human
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VS-10-310-914A-1045309/c
VS-10-310-914A-1045309/c
VS-10-310-914A-1045309, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION uses thereof
FILE OF INVENTION USES 1000.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045309
LENGTH: 22
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100.0%; Pred. No. 0.99;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. c.
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CURRENT FILING DATE: 2002-12-C
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045307
LENGTH: 22
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Best Local Similarity 100.
Matches 22; Conservative
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Matches 22; Conservative
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US-10-310-914A-1045310/c
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US-10-310-914A-1045309
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                                                                   RESULT 32
US-10-914A-1045303/C
US-10-310-914A-1045303/C
Sequence 1045303, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Wiler, Word of novel regulatory genes and TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USES 12002-12-06
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045303
LENGTH: 22
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APPLICANT: Benevich, Isaac
APPLICANT: Baller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: uS/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045306
LENGTH: 22
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100.0%; Pred. No. cot.
0; Mismatches
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 TGTGGGAGAGGCTTAGACCTGAA
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Best Local Similarity 100.
Matches 22; Conservative
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US-10-310-914A-1045306/c
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Best Local Similarity
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US-10-310-914A-1045306
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Sequence 1045319, Application US/10310914A

Publication No. US2006000332A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SHILE OF INVENTION:
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1045319

LENGTH: 22
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
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Pred. No. 0.99;
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100.0%; Pred. No. -
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045315
LENGTH: 22
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Best Local Similarity 100.0
Matches 22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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ORGANISM: Human
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ORGANISM: Human
                                                                                              TYPE: RNA
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUSOI.
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: PatentIn version 3.3
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06697-0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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Pred. No. 0.99;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Preu. ...
                                                                                                            Sequence 1045313, Application US/10310914A; Publication No. U820060003322A1; GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
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APPLICANT: Bentwich, Isaac
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  CTGTGGGAGAGGCTTAGACCTG
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Best Local Similarity 100..
Best Local 22; Conservative
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Matches 22; Conservative
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US-10-310-914A-1045315/c
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                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1045313
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
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LENGTH: 22
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US-10-310-914A-1045332/c

US-10-310-914A-1045332, Application US/10310914A

Sequence 104532, Application US/10310914A

Publication No. US2006000332A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: USES TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SO
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045305
LENGTH: 21
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100.0%; Pred. No. 3.2;
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                                                                                                                                                                                                                Query Match 1.3%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.5 Matches 22; Conservative 0; Mismatches
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SOFTWARE: Patentin version 3.3
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Matches 21; Conservative
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US-10-310-914A-1045305/c
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Best Local Similarity
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                                                                                         TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Human
                          SEQ ID NO 1045330
LENGTH: 22
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT PAPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045329
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Publication No. US20060003322A1
Publication No. US20060003322A1
Publication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICANTON NUMBER: US/10/310,914A
CURRENT APPLICANTON NUMBER: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                             APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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100.0%; Pred. No. 0.99;
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                                                                                                                   Sequence 1045324, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT.
BENTWICH, ISSAC
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Best Local Similarity 100.
Matches 22; Conservative
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US-10-310-914A-1045329/c
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US-10-310-914A-1045330/c
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LENGTH: 22
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US-11-116-881A-205
US-11-116-881A-205
US-11-116-881A-205
US-11-116-881A-205
Publication No. US20060041949A1
GENERAL INFORMATION:
Nielsen, Mark T.
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: 60/665,451
PRIOR APPLICATION NUMBER: 60/665,097
PRIOR PELING DATE: 2005-01-3-24
PRIOR PELING DATE: 2006-01-32
PRIOR PELING DATE: 2006-01-32
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PELING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/503,989
PRIOR PELING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR PELING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR PELING DATE: 2005-10-0-08
PRIOR PELING DATE: 2005-10-08
PRIOR PELIN
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PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR FILING DATE: 1998-02-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 701
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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100.0%; Pred. No. 3.6;
tive 0; Mismatches 0; Indels
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                       ) TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-293
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US-11-116-881A-2005
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US-11-116-881A-992
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                                                                                 Sequence 1045333, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
URRENT FILING DAIR: 2002-12-06
UNUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PAELELING DAIR: Usesion 3.3
SEQ ID NO 1045333
LENGTH: 21
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APPLICANT: Skeiky, Yasir A.
TITLE OF INVENTION: PROSTRE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PROSTRE. US-11/234,786
CURRENT PELING DATE: 2005-09-23
PRIOR APPLICATION NUMBER: US 09/568,857
PRIOR APPLICATION NUMBER: US 09/568,857
PRIOR APPLICATION NUMBER: US 09/536,857
PRIOR APPLICATION NUMBER: US 09/536,857
PRIOR PILING DATE: 2000-05-27
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-07-13
PRIOR PELING DATE: 1999-07-13
PRIOR PELING DATE: 1999-07-13
PRIOR PILING DATE: 1999-07-13
PRIOR PILING DATE: 1999-07-13
PRIOR PILING DATE: 1999-07-13
PRIOR PILING DATE: 1999-04-03
PRIOR PILING DATE: 1999-04-03
PRIOR PILING DATE: 1999-04-03
PRIOR PILING DATE: 1999-04-03
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Pred. No. 3.2;
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100.0%; Pred. No. ...
... 0; Mismatches
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| Sequence 293, Application US/11234786
| Publication No. US20060024301A1
| GENERAL INFORMATION:
| APPLICANT: Xu, Jiangchun
| APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker Susan L. APPLICANT: Jiang, Yudiu
| APPLICANT: Kalos, Michael D. APPLICANT: Reed, Steven G. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Udvick, Thomas S. APPLICANT: Carter, Darrick
| APPLICANT: Carter, Darrick
| APPLICANT: Carter, Darrick
| APPLICANT: Carter, Darrick
| APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Li, SAMUEL X. APPLICANT: Li, SAMUEL X. APPLICANT: 
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Best Local Similarity
Matches 21; Conserval
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ORGANISM: Human
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PEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
COCATION: (37)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40) ... (41)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (73)... (73)
OTHER INFORMATION: n is a, c, g, or t
                          1693 GTACCTCGGCGCGCACCA 1713
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                                                                          24 GTACCTCGGCCGCGACCACGC 4
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Matches 21; Conserva
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                                     APPLICANT: Xu, Dongmei
APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-03-24
PRIOR PLILING DATE: 2005-03-24
PRIOR PELICATION NUMBER: 60/665,097
PRIOR PELICATION NUMBER: 60/665,097
PRIOR PELICATION NUMBER: 60/665,235
PRIOR PELICATION NUMBER: 60/666,235
PRIOR PELICATION NUMBER: 60/666,235
PRIOR PELICATION NUMBER: 10/934,944
PRIOR FILING DATE: 2004-09-03
PRIOR PELICATION NUMBER: 10/934,944
PRIOR PELICATION NUMBER: 60/566,235
PRIOR PELICATION NUMBER: 60/566,235
PRIOR PELICATION NUMBER: 60/665,369
PRIOR PELICATION NUMBER: 60/665,369
PRIOR PELICATION NUMBER: 60/469-03
PRIOR PELICATION NUMBER: 60/489,368
PRIOR PELICATION NUMBER: 60/418,933
PRIOR PELICATION NUMBER: 60/418,933
PRIOR PELICATION NUMBER: 60/418,933
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PRIOR PELICATION NUMBER: 60/418,933
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US-11-057-484A-13/C

Sequence 13, Application US/11057484A

Publication No. US2006002931A1

GENERAL INFORMATION:

APPLICANT: Finkel, Terri H.

APPLICANT: Finkel, Terri H.

TITLE OF INVENTION: Cellular Genes Regulated by HIV-1

TITLE OF INVENTION: Infection and Methods of Use Thereof

FILE REFERENCE: CHOP. 0146CIP

CURRENT APPLICATION NUMBER: US/11/057,484A

CURRENT PILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: US 60/358,803

PRIOR FILING DATE: 2005-02-19

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 13

LENGTH: 509
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100.0%; Pred. No. 3.6;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.6;
tive 0; Mismatches 0; Indels
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Publication No. US20060041949A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.3 SEQ ID NO 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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; ORGANISM: Homo sapien
US-11-057-484A-13
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RESULT 53
US-11-206-587-4/C

Sequence 4, Application US/11206587
Fublication No. US20060040306A1
GENERAL INFORMATION:
TAPLICANT: Leiby, Kevin R.
APPLICANT: Application Section R.
TITLE OF INVENTION: 14534 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND TITLE OF INVENTION: THEREOF APPLICANT: 201-05-08-18
TITLE OF INVENTION: THEREOF SAD COMPOSITIONS OF HUMAN PROTEINS OF HU
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US-11-201-194-5

Sequence 5, Application US/11201194

Publication No. US2066019306A1

SEQUENCE 5.

Publication No. US2066019306A1

SEXERAL INFORMATION:

APPLICANT: University College Cork - National University of Ireland,

APPLICANT: Cork

APPLICANT: Cork

TITLE OF INVENTION: Detection of ochratoxin A producing fungi

FILE REFERENCE: NATI25

CURRENT FILING DATE: 2005-08-11

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.2

LENGTH: 582
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                                                                                                                Sequence 193835, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AMIO1086)

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-06-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 193835

LENGTH: 25
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Publication No. US2005028757041

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM.01086)

CURRENT FILING DATE: 2005-05-25

FRIOR PELLING DATE: 2005-06-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

LENGTH: 25
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11;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 CGGACTCCTGCTGCAAGGAG 570
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Best Local Similarity 100.0
Matches 20; Conservative
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Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial
                                                                             RESULT 56
US-11-136-527-193835/c
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US-11-136-527-193849/c
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APPLICANT: Benewich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 54
US-10-914A-1045308/c
US-10-310-914A-1045308/c
Sequence 1045308, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USES 106097.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 1045308
LENGTH: 20
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                                                                                                                                                                                                        Query Match 1.2%; Score 21; DB 9; Length 1820; Best Local Similarity 100.0%; Pred. No. 3.8; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 20; DB 8; Length 20;
100.0%; Pred. No. 11;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                              1693 GTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1303 GCCCACTCTGGCTCCTG 1322
                                                                                                NAME/KEY: misc_feature

LCCATION: (1)...(1820)

; OTHER INFORMATION: n = A,T,C or G

US-11-206-587-4
                                                                                                                                                                                                                                                                                                                                      27 GTACCTCGGCGGCGACCACGC 7
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
                                     NAME/KEY: CDS
LOCATION: (146)...(1390)
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-310-914A-1045312/c
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US-10-310-914A-1045312
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ORGANISM: Human
                                                                                   FEATURE:
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1418 CCCTTCCTTCCTGCTCATGG 1437

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Gaps
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PRIOR FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: 09/284,782
PRIOR FILING DATE: 1999-0-06
PRIOR FILING DATE: 1997-11-12
PRIOR PELICATION NUMBER: 6,057,111
PRIOR APPLICATION NUMBER: PCT/US97/20989
PRIOR APPLICATION NUMBER: 60/030,549
PRIOR APPLICATION NUMBER: 60/030,549
PRIOR FILING DATE: 1996-11-13
NUMBER OF SEQ ID NOS: 36
SSEQ ID NO 14
LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
| NAME/KEY: misc_feature
| LOCATION: 481, 483, 484, 485, 486
| OTHER INFORMATION: n = A,T,C or G
| US-09-925-065A-613855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 62
US-11-136-527-3780/c
; Sequence 3780, Application US/11136527
                                                                                                                                                                                                                                                                                                                                                                                                                                   1694 TACCTCGGCGCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 TACCTCGGCCGCGACCACGC 24
                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Primer US-11-031-356-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                               ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 61
US-09-925-065A-613855/c
                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                     FEATURE:
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
FURENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 193854
LENGTH: 25
 APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 03.096-04.000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 36.830
SOFTWARE: Patentin version 3.2
SEQ ID NO 193849
LENGTH: 25
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11;
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Publication No. US20050272056A1
GENERAL INFORMATION:
APPLICANT: Quark Biotech Inc.
APPLICANT: Quark Biotech Inc.
TITLE OF INVENTION:
FILE REFERENCE: 65507-F / 003/PCT1-US4
CURRENT APPLICATION NUMBER: US/11/031,356
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 10/704,112
PRIOR APPLICATION NUMBER: 10/704,112
PRIOR APPLICATION NUMBER: 09/499,553
                                                                                                                                                                                                                                                                                                                                         Query Match 1.2%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 11; Matches 20; Conservative 0; Mismatches
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US-11-136-527-193854/c
; Sequence 193854, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                  551 CGGACTCCTGCTGCAAGGAG 570
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Best Local Similarity 100.0
Matches 20, Conservative
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CTHER INFORMATION: Probe
US-11-136-527-193854
                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Probe US-11-136-527-193849
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ORGANISM: Artificial
                                                                                                                                                                                                                                                ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 60
US-11-031-356-14/c
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US-10-750-623-36767
                                                                                                                                               TYPE: DNA
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                                                                   APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031895-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
SOFTWARE: PALENTIN NOS: 362830
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 3780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031996-041000 (AM10.086)
CURRENT PELLING DATE: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 352830
SOFTWARE: Patentin version 3.2
SEQ ID NO 7876
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Publication No. US2005026603A1

GENERAL INFORMATION:

APPLICANT: MI GENOMICS, INC.

APPLICANT: MENSENFELD, Sue K.

APPLICANT: RERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: RAFES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MAILOO-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 12; Length 680;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%; Score 20; DB 12; Length 680;
100.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551 CGGACTCCTGCTAGGAG 570
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Publication No. US20050287570A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Rattus norvegicus
US-11-136-527-3780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Rattus norvegicus
US-11-136-527-7876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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US-10-750-185-36767/c
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RESULT 66
US-11-096-568A-25683/C
US-11-096-568A-25683/C
Sequence 25683, Application US/11096568A
Sequence 25683, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NOS: 34471
LENGTH: 1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILLIOO: LOSSES OF TOTAL CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 65
US-10-750-623-36767/C
; Sequence 35767, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INPORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: ROSENFELD, David
. APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 36767
LENGTH: 993
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 36767
LENGTH: 993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             892 GCTCCTCCTGCCTTGGCTG 873
                                                                                                                                                                                                                                                                                                                                                                                                           892 Gécrécrécerrécere 873
                                                                                                                                                                           ORGANISM: Bovine 19866880507628
US-10-750-185-36767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bovine 19866880507628
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ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1280)
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Sequence 1045325, Application US/10310914A
Publication No. US2066003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bother, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION UNDER: US/10/310,914A
CURRENT APPLICATION UNDER: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045325
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1045311, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, 1800
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
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Publication No. US2066003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT PAPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045334
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100.0%; Pred. No. 35;
tive 0; Mismatches (
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100.0%; Pred. No. 35;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity 100.1
Matches 19; Conservative
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US-10-310-914A-1045334/c
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                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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Sequence 1045321, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045321
LENGTH: 19
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 36-230
SOFTWARE: Patentin version 3.2
SEQ ID NO 3889
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100.0%; Pred. No. ...,
0; Mismatches
; OTHER INFORMATION: Ceres Seq. ID no. 13492847
US-11-096-568A-25683
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1.1%; Score 19; DB E
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches
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US-11-136-527-3889
US-11-136-527-3889
Squence 3889, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
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Best Local Similarity 100.
Matches 20, Conservative
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Matches 20; Conservative
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US-10-310-914A-1045321/c
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US-10-310-914A-1045325/c
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                                                                                                                                                                                                                              APPLICANT: Minature.

APPLICANT: KNOWOVA, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Resholds, Angela
APPLICANT: Marshall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
SRO READ NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430755
LEMENT: NUMBER: MINATURE NOS: 1591911
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1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels
                                                                                                                                             Sequence 1430755, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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APPLICANT: Dharmacon, Inc.
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    1 GGAGACAUAUGAUAAACCA 19
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US-11-101-244-1430755
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; ORGANISM: Homo sapiens
US-11-101-244-1430756
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US-10-310-914A-1045335/c
US-10-310-914A-1045335/c
Sequence 104535, Application US/10310914A
Publication No. US2060003322A1
Hobbitcation No. US2060003322A1
HOBBITCANT: Bentwich, Isaac
APPLICANT: Shiler, Kwizat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REPERENCE: 06087.0200. CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SSEQ ID NO 1045335
LENGTH: 19
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APPLICANT: Chrorova, Anastasia
APPLICANT: Khvorova, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ IN DOS: 1591911
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100.0%; Pred. No. 35;
tive 0; Mismatches 0; Indels
                                                                         Score 19; DB 8; Length 19;
Pred. No. 35;
                                                                                                                       0; Indels
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                                                                                                                                                                 1203 GCCAGGCCCAGCTGCCACA 1221
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Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 84.29
Matches 16; Conservative
; ORGANISM: Human
US-10-310-914A-1045334
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US-11-101-244-1430754
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84.2%;
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Best Local Similarity 84.2'
Matches 16; Conservative
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Matches 14; Conservative
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US-11-101-244-1430759
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sequence 10.244.1430/2),
sequence 10.80757, Application US/11101244
sublication No. U220050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.,
APPLICANT: Khorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reznolds, Angela
APPLICANT: Marchall, William
APPLICANT: Acatinge, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
ITILE OF INVENTION: Functional and Hyperfunctional
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SENGIHAR: Proprietary
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KNOCYOA, Anastasia, APPLICANT: KNOCYOA, Anastasia, APPLICANT: Reymolds, Angela APPLICANT: Leake, Devin APPLICANT: Leake, Devin APPLICANT: Scaringe, Stephen; TITLE OF INVENTION: Functional and Hyperfunctional siRNA; FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430758
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 19; DB 10; Length 19; 78.9%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1430758, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION: APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1455 CATGGAAAGTAAGGAGTTA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           767 TCGATGAGCTGGCCAAGTG 785
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US-11-101-244-1430758
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Best Local Similarity
Matches 15; Conserv
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US-11-101-244-1430758
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Sequence 1430759, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Revnolds, Angela
APPLICANT: Revnolds, Angela
APPLICANT: Revnolds, Angela
APPLICANT: Respective, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502.050
PRIOR APPLICATION NUMBER: 60/502.050
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430759
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1430760, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Characon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Acaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-00-07
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430760

LENGTH: 19
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Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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JS-11-101-244-1430764
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| Sequence 1430761 |
| Sequence 1430761, Application US/11101244 |
| Publication No. US200502467941 |
| CENERAL INFORMATION |
| APPLICANT: Dharmacon, Inc. |
| APPLICANT: Rivorova, Anastasia |
| APPLICANT: Reynolds, Angela |
| APPLICANT: Reynolds, Angela |
| APPLICANT: Responds, Angela |
| APPLICANT: Barshall, William |
| APPLICANT: Barshall, William |
| APPLICANT: Scaringe, Stephen |
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA |
| TITLE OF INVENTION: Public |
| TITLE OF INVENTION |
| PRIOR FILING DATE: 2005-04-07 |
| PRIOR FILING DATE: 2003-09-10 |
| PRIOR FILING DATE: 2003-09-10 |
| PRIOR FILING DATE: 2002-11-14 |
| WUMBER OF SEQ ID NOS: 1591911 |
| SOFTWARE: Proprietary |
| LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.1%; Score 19; DB 10; Length 19; Best Local Similarity 57.9%; Pred. No. 35; Matches 11; Conservative 8; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1430762, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TTTLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Best Local Similarity 78.9
Matches 15; Conservative
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US-11-101-244-1430761
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US-11-101-244-1430762
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Sequence 1430763, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respect Continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued t
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APPLICANT: Dharmacon, Inc.
APPLICANT: Rhvorova, Anastesia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Restinge, Stephen
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430764
LENGTH: 19
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Pred. No. 35;
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Publication No. US20050246794A1
GENERAL INFORMATION:
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AGUAAGGAGUUAGGCAUUA 19
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Matches 13; Conservative
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Matches 14; Conservative
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US-11-101-244-1430763
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RESULT

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APPLICANT: Marchaed, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430767
LENGTH: 19
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Pred. No. 35;
8; Mismatches 0
Sequence 1430767, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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1.1%;
Best Local Similarity 57.9%;
Matches 11; Conservative
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US-11-101-244-1430768
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; ORGANISM: Homo sapiens
US-11-101-244-1430767
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US-11-101-244-1430766

j Sequence 1430766, Application US/11101244

j Publication No. US20550246794A1

j RUDIICALTON No. US20550246794A1

j APPLICANT: Darmacon, Inc.

j APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Searinge, Stephen

j APPLICANT: Soaringe, Stephen

j TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT PILING DATE: 2005-04-07

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 10; Length 19; Pred. No. 35;
                                                                                                                                                                   APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430765
LENGTH: 19
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       US-11-101-244-1430765

Sequence 1430765, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1677 TGACCACAGTTTGTAAGTA 1695
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1.1%;
Best Local Similarity 68.4%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-101-244-1430766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-101-244-1430765
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LENGTH: 19
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Length 19; 0; Indels

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US-11-101-244-1430768

Sequence 1430768, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

PILLE REFERENCE: 13499US
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                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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US-11-101-244-1430769
; Sequence 1430769, Application US/11101244
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RESULT 86 US-11-101-244-1430767

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APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Rescaled, Devin
APPLICANT: Beake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430771
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Pred. No. 3
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
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US-11-101-244-1430771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Homo sapiens
US-11-101-244-1430772
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 92
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                                                       APPLICANT: Khorova, Anastasia
APPLICANT: Khorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Acaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: 06/502,050
PRIOR PLING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 143.0770, Application US/11101244

| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Diarmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Leake, Devin
| APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA
| TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
| FILE REPRENCE: 13499US
| CURRENT FILING DATE: 2005-04-07
| PRIOR PILING DATE: 2003-09-10
| PRIOR FILING DATE: 2003-09-10
| PRIOR FILING DATE: 2003-11-14
| NUMBER OF SEQ ID NOS: 1591911
| SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 10; Length 19;
Pred. No. 35;
2; Mismatches 0; Indels
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57.9%; Pred. No. 35;
tive 8; Mismatches 0; Indels
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US-11-101-244-1430771
Sequence 1430771, Application US/11101244
Publication No. US20050246794A1
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Best Local Similarity 89.5%;
Matches 17; Conservative
Publication No. US20050246794A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 57.9
Matches 11; Conservative
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US-11-101-244-1430769
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ORGANISM: Homo sapiens
US-11-101-244-1430770
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US-11-101-244-1430770
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LENGTH: 19
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SQUTWARE: Proprietary

SQUTWARE: Proprietary

LENGTH: 19
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Pred. No. 35;
3; Mismatches 0
                                                                                                                            Sequence 1430772, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
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; Sequence 1430773, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
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1 GGAGAGACCAGUAAGAUC 19
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
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Gaps
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Sequence 149307/6
Sequence 149307/6
Sublication No. US20050246794A1
Sequence 1497076
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marball, William
APPLICANT: Marball, William
APPLICANT: Caringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
SOFTWARE: Proprietary
SEQ ID NO 1430776
LENGTH: 19
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Ascaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430775
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 10; Length 19;
Pred. No. 35;
9; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%;
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Best Local Similarity 52.69
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1430775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-11-101-244-1430776
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Best Local Similarity
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US-11-101-244-1430777
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; Publication No. US20050246794A1
; Publication No. US20050246794A1
; GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.; APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Barahall, William
    APPLICANT: Barahall, William
    APPLICANT: Scaringe, Stephen
    TITLE OF INVENTION: Functional and Hyperfunctional siRNA
    TURENT APPLICATION NUMBER: US/11/101,244
    CURRENT FILING DATE: 2003-09-10
    PRIOR FILING DATE: 2003-09-10
    PRIOR FILING DATE: 2003-09-10
    PRIOR PLICATION NUMBER: 60/426,137
    PRIOR FILING DATE: 2003-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SOFTHARE: Proprietary
    LENGTH: 19
                                        APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Acachal, william
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFREENCE: 13499UG
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 10; Length 19;
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 19; DB 10; Length 19; 78.9%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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    Dharmacon, Inc.
Khvorova, Anastasia
Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1430773
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US-11-101-244-1430774
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US-11-101-244-1430775
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Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Resynolds, Angela

APPLICANT: Resynolds, Angela

APPLICANT: Resynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Stephen

TILE REFERENCE: 13499US

CURRENT APPLICATION WUMBER: US/11/101,244

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-11-14

SOFTWARE: Proprietary

SEQ ID NO 1430781

LENGTH: 19
           APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
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Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.1%;
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.73
Matches 14, Conservative
Leake, Devin
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                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-101-244-1430780
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; ORGANISM: Homo sapiens
US-11-101-244-1430781
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                                                                                                                                                                                                                                                                                   SEQ ID NO 1430780
LENGTH: 19
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         APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marehall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430777
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Khorova, Anastasia
APPLICANT: Khorova, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marbhall, William
APPLICANT: Marbhall, William
APPLICANT: Marchall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430778
LENGTH: 19
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Pred. No. 35;
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89.5%; Pred. No. 35;
ive 2; Mismatches 0; Indele
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1430778, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION: APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1635 GGAGTTGGTTCTGGTTCTT 1653
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; ORGANISM: Homo sapiens
US-11-101-244-1430777
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Best Local Similarity
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Matches 17; Conserv
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US-11-101-244-1430778
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US-11-101-244-1430780
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### APPLICANT: Marshall, William
### APPLICANT: Scaringe, Stephen
### TITLE OF INVENTION: Functional and Hyperfunctional siRNA
### FILE REPRENCE: 13499US
### CURRENT FILING DATE: 2005-04-07
### CURRENT FILING DATE: 2005-04-07
### PRIOR PILING DATE: 2003-09-10
### PRIOR PILING DATE: 2003-11-14
### PRIOR PILING DATE: 2002-11-14
### NUMBER OF SEQ ID NOS: 1591911
### SOFTWARE: Proprietary
### SOFTWARE: Proprietary
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### SOFTWARE: Proprietary
### ORGANISM: Homo Sapiens
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